

Table 1

<b>EAA</b> (essential amino acids)		<b>NEAA</b> (non-essential amino acids)	
L-arginine·HCl	126.4 mg/l	L-alanine	8.9 mg/l
L-cystine	24.02 mg/l	L-asparagine	13.2 mg/l
L-histidine·HCl·H <sub>2</sub> O	41.92 mg/l	L-aspartic-acid	13.3 mg/l
L-isoleucine	52.46 mg/l	L-glutamic acid	14.7 mg/l
L-leucine	52.46 mg/l	glycine	7.5 mg/l
L-lysine·HCl	73.06 mg/l	L-prolin	11.5 mg/l
L-methionine	14.92 mg/l	L-serine	10.5 mg/l
L-phenylalanine	33.02 mg/l		
L-threonine	47.64 mg/l		
L-tryptophane	10.2 mg/l		
L-tyrosine	36.22 mg/l		
L-valine	46.86 mg/l		

<b>Single amino acids</b>	
histidine·HCl·H <sub>2</sub> O	20 mg/l
isoleucine	50 mg/l
leucine	50 mg/l
methionine	15 mg/l
phenylalanine	15 mg/l
threonine	20 mg/l
tyrosine	20 mg/l
arginine·HCl	240 mg/l
lysine	40 mg/l
D-lysine	40 mg/l
cystine	50 mg/l
tryptophane	5 mg/l
valine	20 mg/l
glutamine	300 mg/l

Table 2. APIT kills different tumor cell lines

models for	kind of tumor	tumor cell line	IC50 (ng/ml)
1. solid tumors	lung cancer	GLC4	9.
	breast cancer	MCF-7, SK-BR-3	*
	prostate cancer	PC3, DU145	*
	colon cancer	HT-29	20
	cervix cancer	HeLa, Chang	* 10
	uterus carcinoma	Hec-1-B	*
	larynx cancer	HEp-2	*
	stomach cancer	AGS	*
	liver cancer	Hep G2	*
2. leukemia	T cell leukemia (ALL)	Jurkat neo	3.2
	T cell leukemia (ALL)	CEM neo	5.6
	B cell leukemia	SKW neo	3
	Monocyte leukemia (AML)	Mono Mac 6	*
	Monocyte leukemia (AML)	THP-1	10
3. "orphan" tumors	Ewings sarcoma	RDES	4.5
		A673	5
4. apoptosis resistant tumors	(CML)	K562	4.25
	T cell leukemia (ALL)	Jurkat Bcl-2	2.7
	T cell leukemia (ALL)	CEM Bcl-X <sub>L</sub>	4.0
	B cell leukemia	SKW Bcl-2	5.5
5. MDR tumors	Lung cancer	GLC4-ADR	10

Table 3. Proteome analysis

Description	gi	NCBI	NCBI version	swissprot	effect
Addolase A (E.C.4.1.2.13)	229674	1ALD	1ALD	P04075	-
26S proteasome regulatory chain 12	2134660	S65491	S65491	-	-
3-Hydroxyacyl-CoA dehydrogenase	2078327	AAB54008	AAB54008.1	Q16836	-
C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase)	115206	P11586	P11586	P11586	-
Chain A, Structure Of Human Glutamate Dehydrogenase-Apo Form or Glutamate dehydrogenase 1	20151189	1L1F_A	1L1F_A	-	m
Cleavage and polyadenylation specific factor 5, 25 kD subunit	4885281	NP_005262	NP_005262.1	P00367	-
Cofilin 1	5901926	NP_008937	NP_008937.1	-	-
Coronin, actin binding protein, 1A	5031635	NP_005498	NP_005498.1	P23528	-
Dihydrolipoamide dehydrogenase precursor; E3 component of pyruvate dehydrogenase	5902134	NP_009005	NP_009005.1	P31146	+
Dihydrolipoamide dehydrogenase precursor; E3 component of pyruvate dehydrogenase	4557525	NP_000099	NP_000099.1	P09622	-
dj553F4.4 (Novel protein similar to <i>Drosophila</i> CG8055 protein)	12314022	CAC14088	CAC14088.1	-	-
DNA replication licensing factor MCM4	1705520	-	-	P33991	+
Elongation factor 1-delta (EF-1-delta)	20141357	P29692	P29692	P29692	-
Enolase 1, alpha; phosphopyruvate hydratase	4503571	NP_001419	NP_001419.1	Q05524	+
Glyceraldehyde-3-phosphate dehydrogenase or uracil DNA glycosylase	31645	CAA25833	CAA25833.1	P04406*	+
Heat shock 60kD protein 1 (chaperonin)	35053	CAA37794	CAA37794.1	P04406*	-
Heat shock 60kDa protein 1 (chaperonin)	14603309	AAH10112	AAH10112.1	Q96FZ6	-
Heat shock 70kD protein 9B (mortalin-2)	4504521	NP_002147	NP_002147.1	P10809	-
Heat shock 70kD protein 9B (mortalin-2)	4758570	NP_004125	NP_004125.1	Q8N1C8	-
Heterogeneous nuclear ribonucleoprotein C, isoform b	4758544	NP_004491	NP_004491.1	P07910	m
Hspc117	6841456	AAF29081	AAF29081.1	Q9P037	m
Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2)	124419	P12268	P12268	P12268	+
Isocitrate dehydrogenase 3 (NAD <sup>+</sup> ) alpha	5031777	NP_005521	NP_005521.1	P50213	-
KH-type splicing regulatory protein (FUSE binding protein 2)	4504865	NP_003676	NP_003676.1	-	-
Nuclear matrix protein NMP200 related to splicing factor PRP19	7657381	NP_055317	NP_055317.1	Q9UMS4	-
Nucleobindin 2	4826870	NP_005004	NP_005004.1	P80303	-
54 kDa nuclear RNA- and DNA-binding protein (p54(nrb)) (p54(nrb))	13124797	Q15233	Q15233	Q15233	+
Peroxiredoxin 1 (Thioredoxin peroxidase 2)	548453	Q06830	Q06830	Q06830	m
Peroxiredoxin 1; Proliferation-associated gene A; proliferation-associated gene A	4505591	NP_002565.1	NP_002565.1	Q06830	m

Table 3. Continuation I

Description	gi	NCBI	NCBI version	swissprot	effect
Peroxiredoxin 2 (Thioredoxin peroxidase 1)	2507169	P32119	P32119	P32119	+
Peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide reductase precursor	5802974	NP_006784	NP_006784.1	P30048	-
2-phosphopyruvate-hydrolase alpha-enolase; carbonate dehydratase	693933	CAA59331	CAA59331.1	P06733	+
Proteasome subunit alpha type 7	12643540	O14818	O14818	O14818	+
Proteasome subunit beta type 1 (Proteasome component C5) (Macropain subunit C5)	130853	P20618	P20618	P20618	+
Ras-GTPase-activating protein SH3-domain-binding protein; GAP binding protein	50311703	NP_005745.1	NP_005745.1	Q13283	m
Replication protein A2, 32kDa	4506585	NP_002937	NP_002937.1	P15927	-
Rho GDP-dissociation Inhibitor 2 (Rho GDI 2) (Rho-GDI bêta) (Ly-GDI)	1707893	P52566	P52566	P52566	-
Ribosomal protein P0; 60S acidic ribosomal protein P0 or similar BLOCK 23	45066667	NP_000993	NP_000993.1	P05388	-
Ribosomal protein, large, P0	20536934	XP_165448	XP_165448.1	Q8NHW5	
RNA-binding protein regulatory subunit	12654583	AAH01127	AAH01127.1	P05388	-
RNA-binding protein regulatory subunit	6005749	NP_009193	NP_009193.1	O14805	+
Semenogelin I; Semenogelin	12720028	XP_001707	XP_001707.2	O14805	+
Similar to villin 2 (ezrin)	4506883	NP_002998	NP_002998.1	P04279	-
Splicing factor proline/glutamine rich (poly)pyrimidine tract binding protein associated)	15530243	AAH13903	AAH13903.1	P15311	-
Stathmin 1; metablastin; prosolin; oncoprotein 18; phosphoprotein 19; leukemia-associated phosphoprotein p18	4826998	NP_005057	NP_005057.1	P23246	-
U2 small nuclear ribonucleoprotein A' (U2 snRNP-A')	134094	P09661	P09661	P09661	+
Vimentin	4507895	NP_003371	NP_003371.1	P08670	-
Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2)	1172554	P45880	P45880	P45880	-

Table 4. Transcriptome analysis

Unigene cluster	Description	GENE	gi	pir/NCBI/swissprot	effect
Hs.3833	3'-phosphoadenosine 5'-phosphosulfate synthase 1	PAPSS1	4885537	NP_005434.1	-
Hs.166563	replication factor C (activator 1) 1, 145kDa	RFC1	15011931	ref:NP_002904.2	-
Hs.78991	DNA segment, numerous copies, expressed probes (GS1 gene)	DXF68S1E	6912346	ref:NP_036212.1	-
Hs.326035	early growth response 1	EGR1	119242	sp:P18146	++
Hs.10885	collagen, type VI, alpha 1	COL6A1	15011913	ref:NP_001839.1	++
Hs.78944	regulator of G-protein signalling 2, 24kDa	RGS2	2135146	pir:J53020	++
Hs.110571	growth arrest and DNA-damage-inducible, beta	GADD45B	9945332	ref:NP_056490.1	++
Hs.78465	v-jun sarcoma virus 17 oncogene homolog (avian)	JUN	135298	sp:PO5412	+
Hs.82646	DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	1706473	sp:J25685	+
Hs.169840	TTK protein kinase	TTK	346403	pir:AA42861	+
Hs.211601	mitogen-activated protein kinase kinase kinase 12	MAP3K12	18202489	sp:Q12852	+
Hs.345728	suppressor of cytokine signalling 3	SSI-3	4507235	ref:NP_003946.1	+
Hs.3776	zinc finger protein 216	ZNF216	5174755	ref:NP_005998.1	+
Hs.73037	cannabinoid receptor 2 (macrophage)	CNR2	450068	pir:1920360A	+
Hs.167578	ESTTFLJ25357 hypothetical protein FLJ25357		740170	2004399A	+
Hs.8715	hypothetical protein MGC3232	MGC3232	3024681	sp:O002668	+
Hs.74520	spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	SCA1	1082237	pir:S46268	+
Hs.6151	pumilio homolog 2 (Drosophila)	PUM2	14277945	pdb:1IB3	+
Hs.8026	EST, Highly similar to SES2 HUMAN Sesitin 2 [H.sapiens]		136333882	sp:J58004	+
Hs.82173	TGFB Inducible early growth response	TIEG	11387050	sp:Q13118	+
Hs.198307	von Hippel-Lindau binding protein 1	VBP1	4507873	ref:NP_003363.1	+
Hs.179982	tumor protein p53-binding protein	TP53BP1	5032191	ref:NP_005793.1	+
Hs.2549	adrenergic, beta-3-, receptor	ADRB3	1070630	pir:QRHUBE	+
Hs.2128	dual specificity phosphatase 5	DUSP5	12707566	ref:NP_004410.2	+
Hs.36927	heat shock 105kD	HSP105B	5729879	ref:NP_006635.1	+
Hs.77558	high mobility group nucleosomal binding domain 3	HMGN3	2495254	sp:Q15651	+
Hs.460	activating transcription factor 3	ATF3	88875	pir:C34223	+
Hs.104125	adenylyl cyclase-associated protein	CAP	399184	sp:Q01518	+
Hs.24719	modulator of apoptosis 1	MAP-1	11545896	ref:NP_071434.1	+
Hs.8257	cytokine inducible SH2-containing protein	CISH	13124022	sp:Q9NSE2	+
Hs.101383	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments)		2135765	pir:A43932	+

Table 4. Continuation 1

Unigene cluster	Description	GENE	gi	pir/NCBI/swissprot effect
Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	CDW52	4502761	ref:NP_001794.1 +
Hs.8084	hypothetical protein dj465N24.2.1	DJ465N24.2.1	10092679	ref:NP_064713.1 +
Hs.78829	ubiquitin specific protease 10	USP10	11360280	pir:T47164 +
Hs.889	Charot-Leyden crystal protein	CLC	11942631	pdb:1LCL +
Hs.277401	bromodomain adjacent to zinc finger domain, 2A	BAZ2A	7304921	ref:NP_038477.1 +
Hs.300863	lethal (3) malignant brain tumor (l(3)mbt protein (Drosophila) homolog	H-L(3)MBT	14141728	ref:NP_056293.2 +
Hs.45552	ubiquillin 2	UBQLN2	16753207	ref:NP_038472.2 +
Hs.151903	GrpE-like protein cochaperone	HMG-E	18202951	sp:Q9HAV7 +
Hs.36606	EST, Weakly similar to T29982 hypothetical protein F11G11.12; [C. elegans]			+ +
Hs.85302	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	ADARB1	2829669	sp:P78563 +
Hs.113823	CipX caseinolytic protease X homolog (E. coli)	CLPX	14916956	sp:Q76031 +
Hs.25911	HLA-B associated transcript 2	BAT2	18375626	ref:NP_542417.1 +
Hs.95821	osteoclast stimulating factor 1	OSTF1	11134088	sp:Q92882 +
Hs.11217	KIAA0877 protein	KIAA0877		+ +
Hs.301064	arafaptin 1	HSU52521	1703203	sp:P53367 +
Hs.276238	EST, Moderately similar to kinase suppressor of ras [Mus musculus]			+ +
Hs.211569	G protein-coupled receptor kinase 5	GPRK5	2135145	pir:A48277 +
Hs.25524	protein tyrosine phosphatase, non-receptor type 23	PTPN23	7512735	pir:T14756 +
Hs.94498	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2	5803068	ref:NP_006857.1 +
Hs.24427	DKFZP566C1646 protein	DC8	7512839	pir:T08737 +
Hs.46	platelet-activating factor receptor	PTAFR	107346	pir:A40191 +
Hs.90800	EST, Highly similar to matrix metalloproteinase 16, isoform 1; membrane-type matrix metalloproteinase 3; membrane-type-3 matrix metalloproteinase [Homo sapiens]		13027802	ref:NP_005932.2 +
Hs.81648	hypothetical protein FLJ11021 similar to splicing factor, arginin/serine-rich 4	FLJ11021	2833266	sp:Q15696 +
Hs.80338	Bcl-2-associated transcription factor	BTF	7661958	ref:NP_055554.1 +
Hs.238407	EST, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]		8923452	ref:NP_060312.1 +
Hs.154668	KIAA039 - gene product	KIAA0391	3024899	sp:Q15091 +
Hs.76666	chromosome 9 open reading frame 10	C9orf10	13431358	sp:Q9NZB2 +
Hs.9701	growth arrest and DNA-damage-inducible, gamma	GADD45G	5729836	ref:NP_006696.1 +
Hs.100527	connector enhancer of KSR2	CNK2	7662368	ref:NP_055742.1 +
Hs.777274	plasminogen activator, urokinase	PLAU	224665	pir:1110198A +

Table 4. Continuation II

Unigene cluster	Description	GENE	gi	pir/NCBI/swissprot	effect
Hs.93516	ESTs				+
Hs.376709	Homo sapiens cDNA FLJ33768 fis, clone BRH1P20000021				+
Hs.110299	mitogen-activated protein kinase kinase 7	MAP2K7	4826946	ref:NP_005034.1	+
Hs.31396	ESTs, weakly similar to S28807 collagen alpha 1(X) chain precursor [M.musculus]				+
Hs.129715	gonadotropin-releasing hormone 2	GNRH2	3913735	sp:O43555	+
Hs.169370	FYN oncogene related to SRC, FGR, YES	FYN	125370	sp:P06241	+
Hs.82007	methionyl aminopeptidase 1	METAP1	1703270	sp:P53582	+
Hs.239018	RAB11B, member RAS oncogene family	RAB11B	1082426	pir:JC2487	+
Hs.126852	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	SLC6A13	7705539	ref:NP_057699.1	+

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Table 5. Transcriptome analysis

GENBANK	GENENAME	SYMBOL	EFFECT
NM_005252	v-fos FBJ murine osteosarcoma viral oncogene homolog	FOS	++
NM_006705	growth arrest and DNA-damage-inducible, gamma	GADD45G *	++
NM_001964	early growth response 1	EGR1	++
NM_002228	v-jun sarcoma virus 17 oncogene homolog (avian)	JUN	++
NM_015675	growth arrest and DNA-damage-inducible, beta	GADD45B *	++
NM_001124	adrenomedullin	ADM	++
NM_005346	heat shock 70kDa protein 1B	HSPA1B	++
NM_002166	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	ID2	++
NM_004417	dual specificity phosphatase 1	DUSP1	++
NM_003745	suppressor of cytokine signaling 1	SOCS1	++
NM_002923	regulator of G-protein signalling 2, 24kDa	RGS2	*
NM_005627	serum/glucocorticoid regulated kinase	SGK	++
BC012321	activity-regulated cytoskeleton-associated protein	ARC	++
NM_025195	phosphoprotein regulated by mitogenic pathways	C8FW	+
NM_030751	transcription factor 8 (represses Interleukin 2 expression)	TCF8	+
NM_014330	protein phosphatase 1, regulatory (inhibitor) subunit 15A	PPP1R15A	+
NM_004083	DNA-damage-inducible transcript 3	DDIT3	+
NM_001841	cannabinoid receptor 2 (macrophage)	CNR2	*
NM_004024	activating transcription factor 3	ATF3	+
NM_001706	B-cell CLL/lymphoma 6 (zinc finger protein 51)	BCL6	+
NM_004428	ephrin-A1	EFNA1	+
NM_004419	dual specificity phosphatase 5	DUSP5	+
NM_003088	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	FSCN1	+
AB014566	dishevelled associated activator of morphogenesis 1	DAAM1	+
NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1	*
NM_004962	growth differentiation factor 10	GDF10	+
D7994	kidney ankyrin repeat-containing protein	KANK	+
NM_006301	mitogen-activated protein kinase kinase 12	MAP3K12 *	+
NM_002928	regulator of G-protein signalling 16	RGS16	+
NM_003955	suppressor of cytokine signaling 3	SOCS3	+
NM_004430	early growth response 3	EGR3	+
NM_001731	B-cell translocation gene 1, anti-proliferative	BTG1	+
NM_012342	putative transmembrane protein	NMA	+
NM_002262	killer cell lectin-like receptor subfamily D, member 1	KLRD1	+
NM_006007	zinc finger protein 216	ZNF216 *	+
NM_000905	neuropeptide Y	NPY	+

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Table 5. (continued) Transcriptome analysis

GENBANK	GENENAME	SYMBOL	EFFECT
NM_004418	dual specificity phosphatase 2	DUSP2	+
NM_031459	sestrin 2	SES2	+
AF332558	BCL2 binding component 3	BBC3	+
NM_006000	tubulin, alpha 1 (testis specific)	TUBA1	+
NM_006644	heat shock 105kDa protein 1	HSPH1	+
L24498	growth arrest and DNA-damage-inducible, alpha	GADD45A	+
AK024029	modulator of apoptosis 1	MOAP1	+
NM_005409	chemokine (C-X-C motif) ligand 11	CXCL11	+
NM_003383	very low density lipoprotein receptor	VLDLR	+
AF267856	hypothetical protein dj465N124.2.1	DJ465N124.2.1	+
NM_002450	metallothionein 1L	MT1L	+
NM_001828	Charot-Leyden crystal protein	CLC	+
NM_013370	pregnancy-induced growth inhibitor	OKL38	+
AB014581	(3)mbt-like (Drosophila)	L3MBTL	+
NM_006875	pim-2 oncogene	PIM2	+
AL031665	actin, gamma pseudogene 3	ACTGP3	+
AI985514	ribosomal protein S19	RPS19	+
NM_080686	HLA-B associated transcript 2	BAT2	+
NM_021184	chromosome 6 open reading frame 47	C6orf47	+
NM_015471	DKFZP566O1646 protein	DC8	+
NM_000952	platelet-activating factor receptor	PTAFR	+
BC012625	protein phosphatase 1, regulatory (inhibitor) subunit 3C	PPP1R3C	+
NM_023012	hypothetical protein FLJ11021 similar to splicing factor, aiginine/serine-rich 4	FLJ11021	*
AK024358	macrophage expressed gene 1	LOC219972	+
NM_002658	plasminogen activator, urokinase	PLAU	*
U12767	nuclear receptor subfamily 4, group A, member 3	NR4A3	+
NM_016615	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	SLC6A13	+
NM_002135	nuclear receptor subfamily 4, group A, member 1	NR4A1	+
AJ251595	CD44 antigen (homing function and Indian blood group system)	CD44	-
NM_005433	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	YES1	-
NM_006325	RAN, member RAS oncogene family	RAN	-
NM_004775	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	B4GALT6	-
AK056671	upstream regulatory element binding protein 1	UREB1	-
NM_022817	period homolog 2 (Drosophila)	PER2	-
L07044	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	CAMK2G	-
NM_014890	downregulated in ovarian cancer 1	DOC1	-

Table 5. (continued) Transcriptome analysis

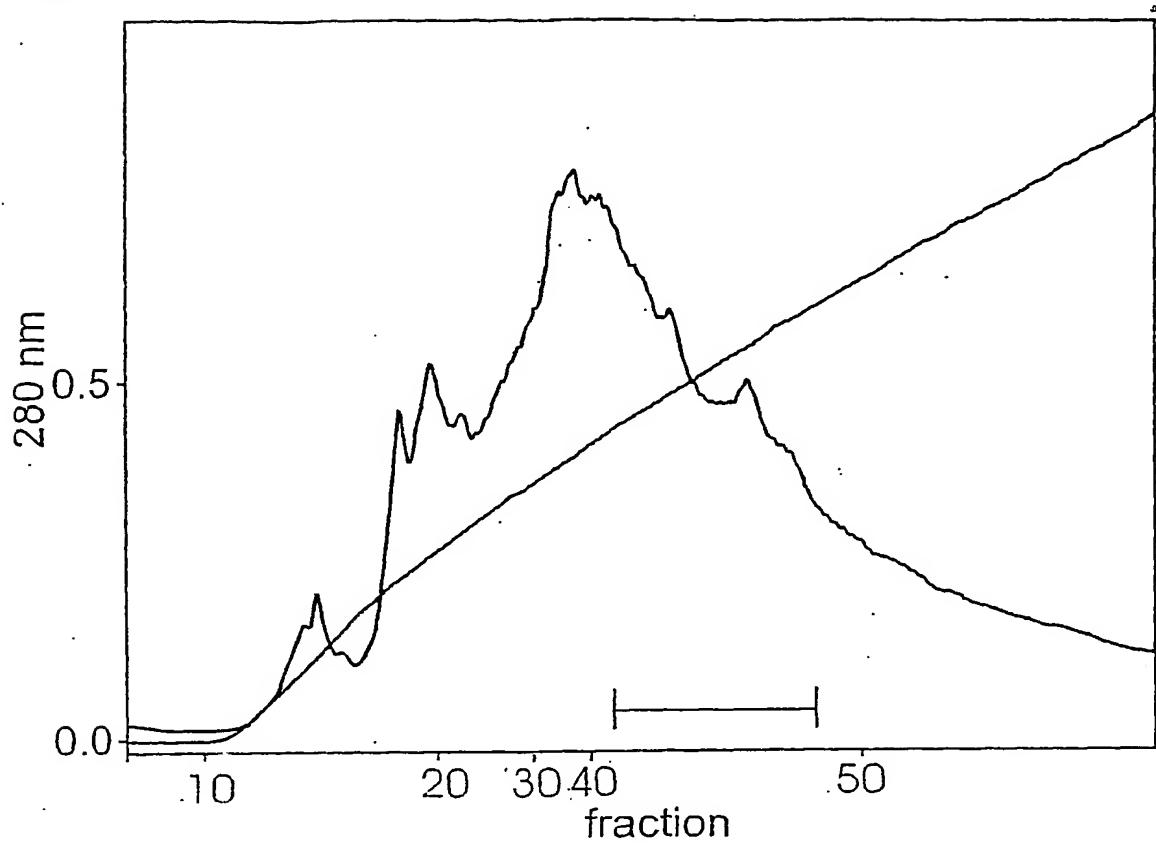
GENBANK	GENENAME	SYMBOL	EFFECT
NM_001782	CD72 antigen	CD72	
NM_005766	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	FARP1	
NM_000566	Fc fragment of IgG, high affinity Ia, receptor for (CD64)	FCGR1A	
NM_003036	v-ski sarcoma viral oncogene homolog (avian)	SKI	
NM_001713	betaine-homocysteine methyltransferase	BHMT	
NM_001682	ATPase, Ca++ transporting, plasma membrane 1	ATP2B1	
NM_003985	tyrosine kinase, non-receptor, 1	TNKA1	
NM_004752	glial cells missing homolog 2 (Drosophila)	GCM2	
BC001619	aldehyde dehydrogenase 1 family, member B1	ALDH1B1	
NM_002422	matrix metalloproteinase 3 (stromelysin 1, progelatinase)	MMP3	
NM_003024	intersecitin 1 (SH3 domain protein)	ITSN1	
NM_002613	3-phosphoinositide dependent protein kinase-1	PDPK1	
NM_000098	carnitine palmitoyltransferase II	CPT2	
BC002712	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	MYCN	
NM_003112	Sp4 transcription factor	SP4	
NM_012062	dynamin 1-like	DNM1L	
NM_000880	Interleukin 7	IL7	
NM_004564	PET112-like (yeast)	PET112L	
NM_001771	CD22 antigen	CD22	
AA904067	protein phosphatase 1, regulatory (inhibitor) subunit 12B	PPP1R12B	
NM_001633	alpha-1-microglobulin/bikunin precursor	AMBp	
NM_007216	Hermansky-Pudlak syndrome 5	HPSS5	
AV708310	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha Isoform	PPP2CA	
AF296765	cerebral cavernous malformations 1	CCM1	
AF155117	kinesin family member 21A	KIF21A	
NM_002006	fibroblast growth factor 2 (basic)	FGF2	
NM_004362	calmodulin	CLGN	
NM_021221	lymphocyte antigen 6 complex, locus G5B	LY6G5B	
AK001541	secretory carrier membrane protein 1	SCAMP1	
HO8291	acid phosphatase 1, soluble	ACP1	
NM_014636	Rai guanine nucleotide exchange factor RaiGpS1A	RAIGPS1A	
NM_053006	serine/threonine kinase 22B (spermogenesis associated)	STK22B	
NM_000220	potassium inwardly-rectifying channel, subfamily J, member 1	KCNJ1	
NM_000633	B-cell CLL/lymphoma 2	BCL2	
NM_003605	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	OGT	

Table 5. (continued) Transcriptome analysis

GENBANK	GENENAME	SYMBOL	EFFECT
NM_006114	translocase of outer mitochondrial membrane 40 homolog (yeast)	TOMM40	-
NM_013404	mesothelin	MSLN	-
NM_020974	signal peptide, CUB domain, EGF-like 2	SCUBE2	-
NM_000439	protein convertase subtilisin/kexin type 1	PCSK1	-
NM_002035	follicular lymphoma variant translocation 1	FVT1	-
AL136924	Ras and Rab interactor 2	RIN2	-
NM_006020	alkB, alkylation repair homolog (E. coli)	ALKBH	-
NM_005433	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	YES1	-
NM_003423	zinc finger protein 43 (HTF6)	ZNF43	-
AF056490	phosphodiesterase 8A	PDE8A	-
NM_033480	F-box only protein 9	FBXO9	-
NM_022789	Interleukin 17E	IL17E	-
NM_007150	zinc finger protein 185 (LM domain)	ZNF185	-
NM_017450	BAI1-associated protein 2	BAIAP2	-
AB037762	myelin expression factor 2	MYEF2	-
NM_003263	toll-like receptor 1	TLR1	-
NM_001089	ATP-binding cassette, sub-family A (ABC1), member 3	ABCA3	-
NM_018240	Ikin of IRRE like (Drosophila)	KIRREL	-
NM_003827	N-ethylmaleimide-sensitive factor attachment protein, alpha	NAPA	-
NM_003569	syntaxis 7	STX7	-
AB046797	KIAA1577 protein	KIAA1577	-
AV723914	hypothetical protein LOC164729	LOC164729	-
NM_015967	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	PTPN22	-
AB007892	CDC25 cell division cycle 5-like (S. pombe)	CDC25L	-
NM_022907	hypothetical protein FLJ23053	FLJ23053	-
NM_004379	cAMP responsive element binding protein 1	CREB1	-
AB023198	KIAA0981 protein	KIAA0981	-
NM_024958	chromosome 20 open reading frame 98	C20orf98	-
NM_001186	BTB and CNC homology 1, basic leucine zipper transcription factor 1	BACH1	-
NM_014639	KIAA0372 gene product	KIAA0372	-
NM_024641	mannosidase, endo-alpha	MANEA	-
AK056671	upstream regulatory element binding protein 1	UREB1	-
NM_003618	mitogen-activated protein kinase kinase kinase 3	MAP4K3	-
NM_005443	3'-phosphoadenosine 5'-phosphosulfate synthase 1	PAPSS1 *	-
NM_022781	ring finger protein 38	RNF38	-
NM_003874	CD84 antigen (leukocyte antigen)	CD84	-

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GENBANK	GENENAME	SYMBOL	EFFECT
NM_000091	collagen, type IV, alpha 3 (Goodpasture antigen)	COL4A3	
NM_000160	glucagon receptor	GCGR	
NM_005019	phosphodiesterase 1A, calmodulin-dependent	PDE1A	
NM_012080	family with sequence similarity 16, member A, X-linked	FAM16AX	

Fig.  
1A

1B

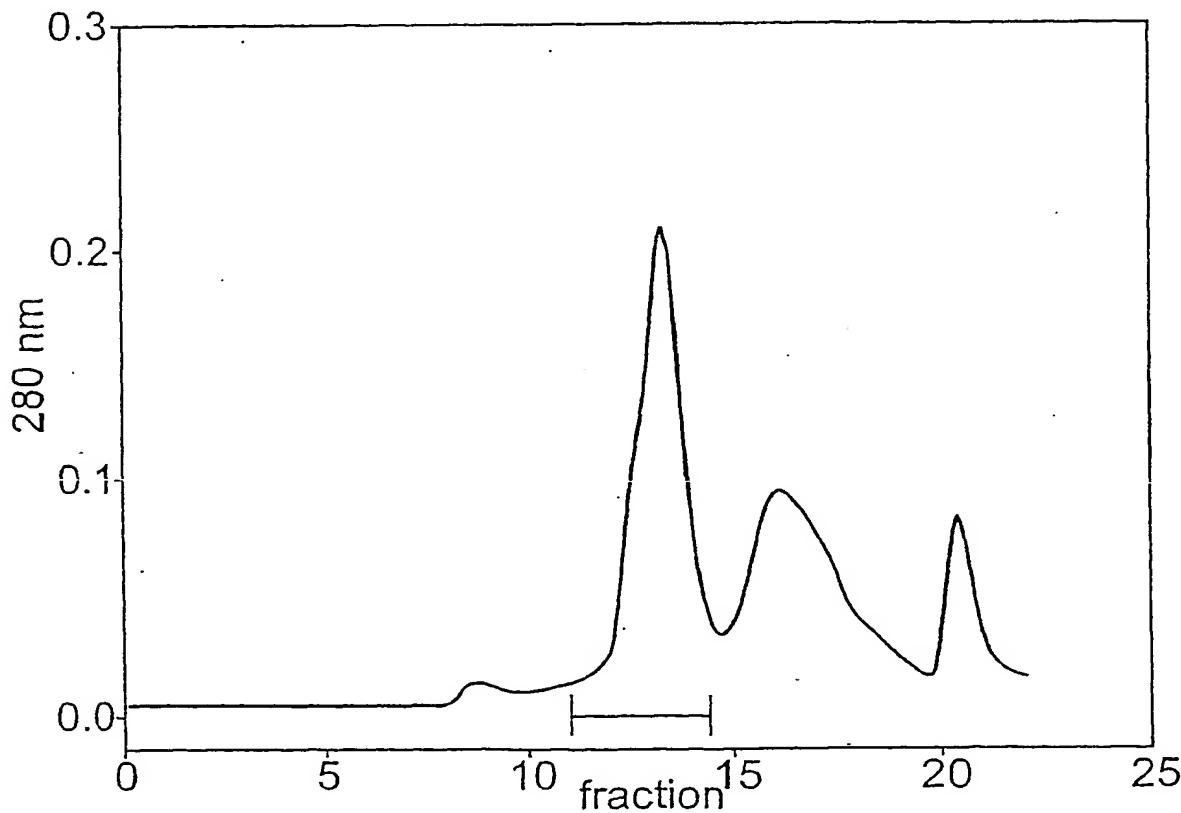
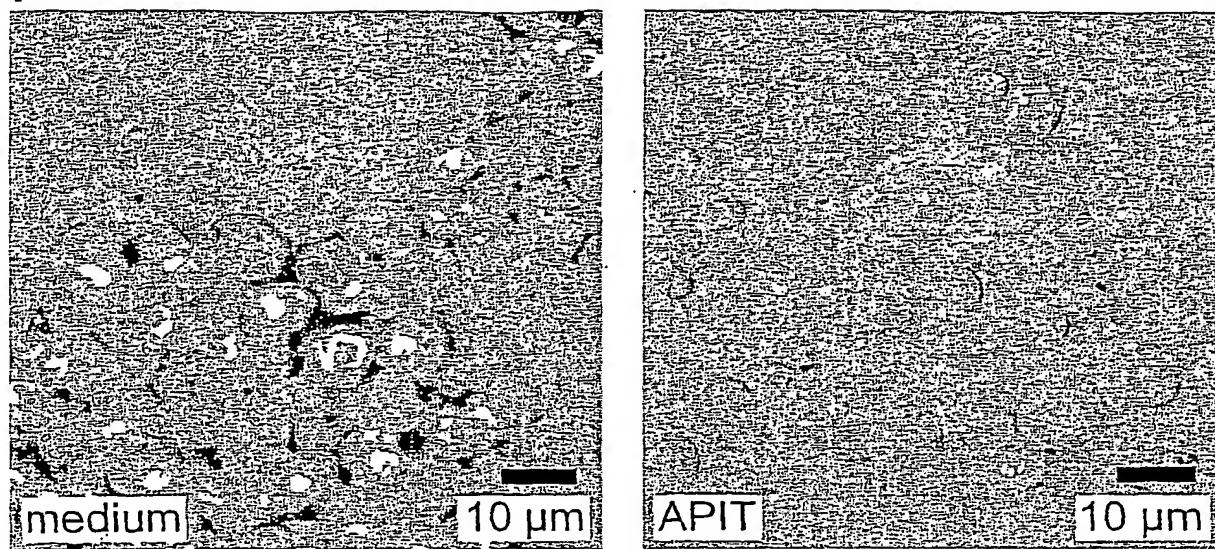
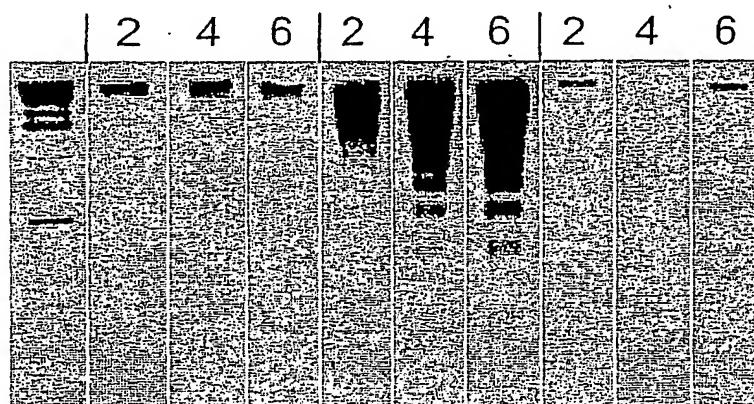


Fig.

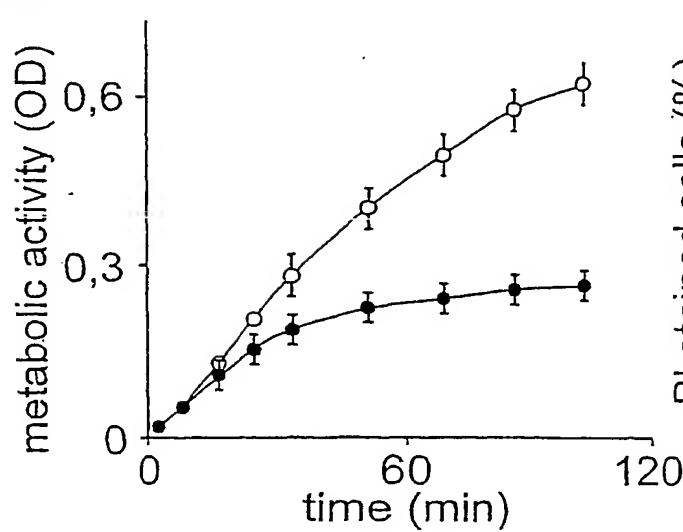
2A



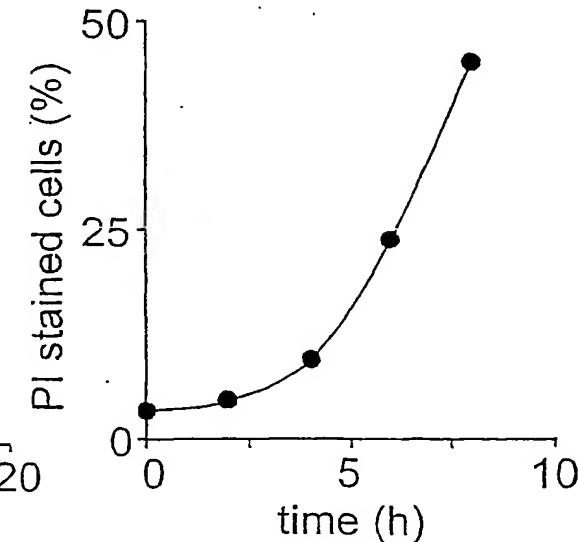
2B m control chx ink



2C



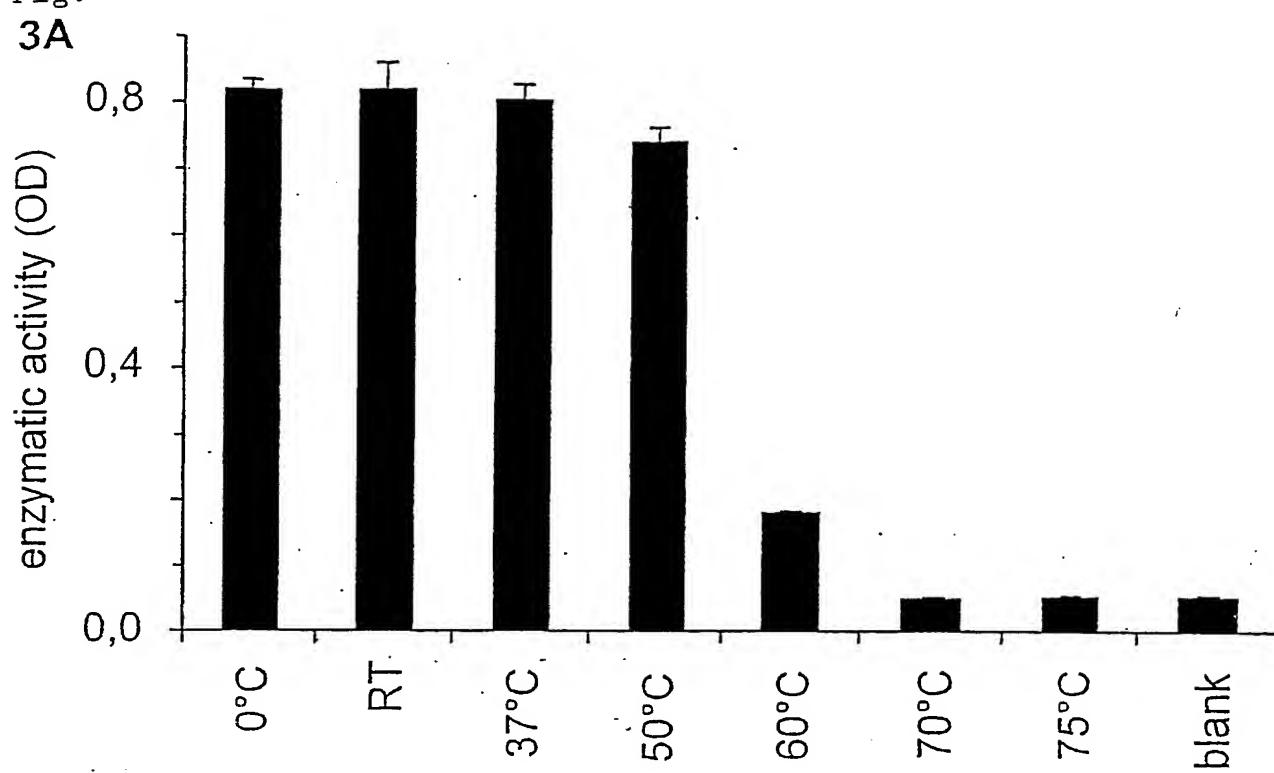
2D



10/15/2007

Fig.

3A



3B

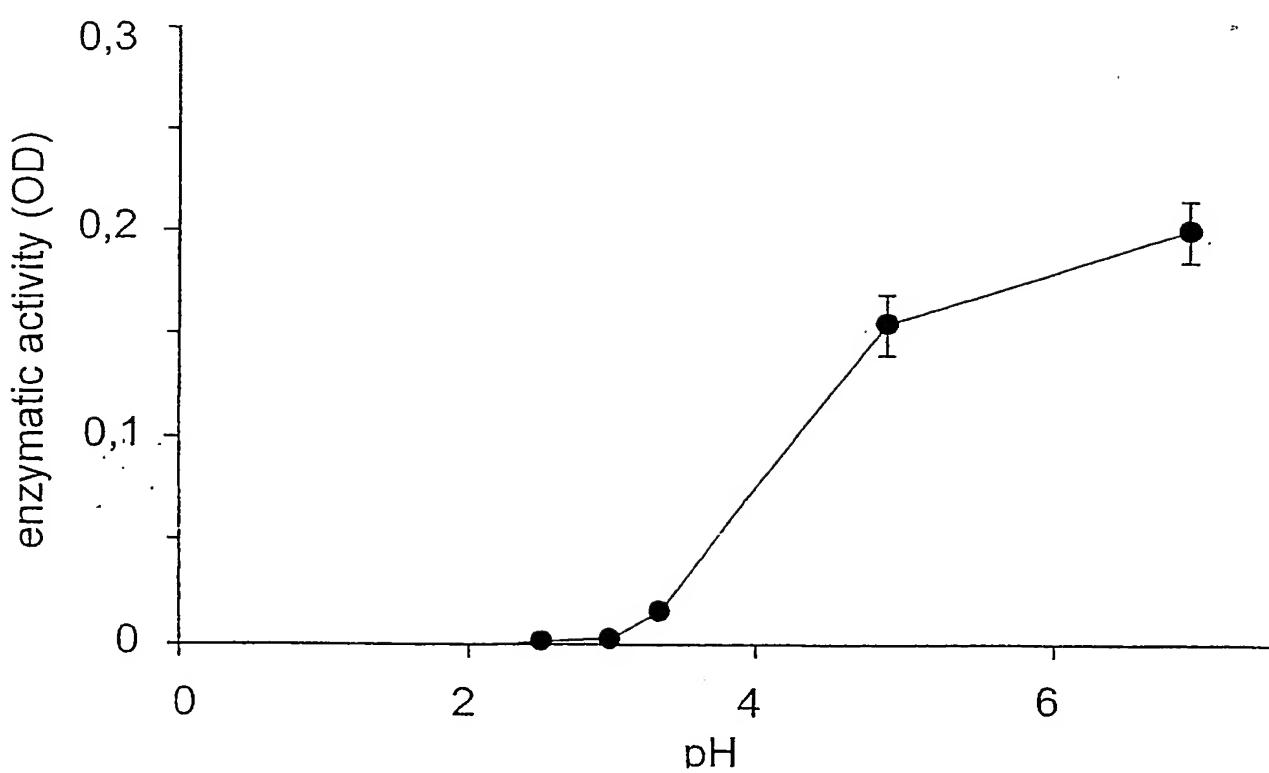


Fig.

3C

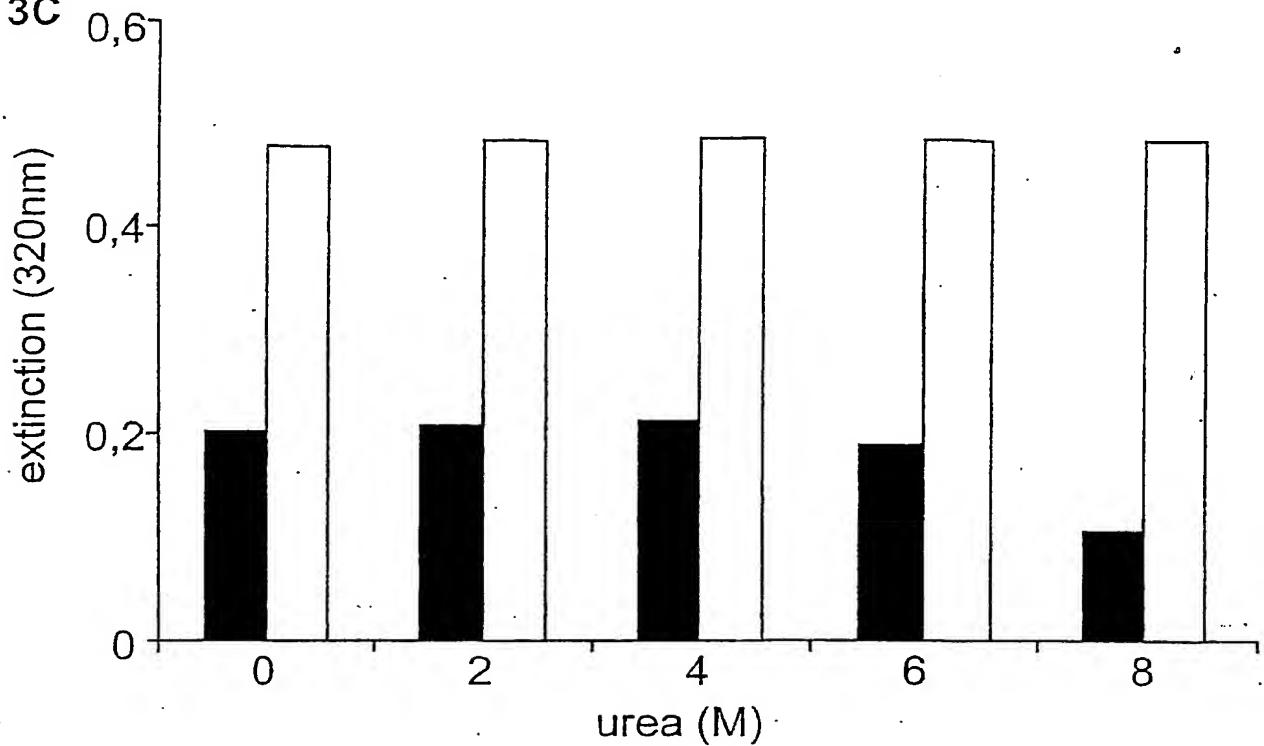


Fig.  
4A

N-terminal sequence:

D-G-I-C-R-N-Q-R-Q  
Q V R PInternal peptide sequences

	Sequence
1	<b>DSGLDIAVFEYSDR</b>
2	<b>LFXYQLPNTPDVNLEI</b>
3	<b>VISELGLTPK</b>
4	<b>XGDVPYDLSPEEK</b>
5	<b>VILAXPVYALN</b>
6	<b>ATQAYAAVRPIPASK</b>
7	<b>VFMTFDQP</b>
8	<b>SDALFFQMYD</b>
9	<b>SEASG DYILIASYADGLK</b>
10	<b>NQGEDIPGS DPQYNQVTEP(L)(K)</b>

X = not determinable

underlined: primer sequence for RT-PCR

Fig.

4B

1	Oligo-dT DBuTag1	tcc taa cgt agg tct aga cct gtt gca ttt ttt ttt ttt ttt ttt
2	V-Fey 3 DTS 5'	tc qtq ttc qar tac tci qay cq
3	DBuTag1 DTS 3'	ctq tag qtc tag acc tgt tgc a
4	ATF Race 3' 660	ccg tgt aga tct cac tgc cat a
5	Abriged Anchor Primer	ggc cac gcg tcg act agt acg ggi igg gii gqq iiq
6	ATF Race 3' 436	ccg ttq aqt tgt aga cct
7	AUAP-EcoRI	aatt ggc cac gcg tcg act agt ac
8	ATF 5' Sign Eco RI GEX/ET	aa ttc tcg tct gct gtg ctt ctc ct
9	ATF 3' Xhol	gac tta gag gaa gta gtc gtt qa

Fig.

4C

M S S A V L L L A C A L V I S V H A D G I **IV** C  
 ATGTCGTCGCTGTGCTTCTCCTGGCTTGTGCGTTGGTATCTCTGTCCACGCCGACGGTATCTGC  
 ... TCGTCTGCTGTGCTTCTCCTGGCTTGTGCGTTGGTATCTCTGTCCACGCCGACGGT **G** TCTGC  
 GACGGTATCTGC  
 R N R R Q C N R E V C G S T Y D **V** A V V G A  
 AGAAACAGACGTCAATGTAACAGAGAGGGTGTGCGGTTCTACCTACGATGTGGCGTGGGGCG  
 AGAAACAGACGTCAATGTAACAGAGAGGGTGTGCGGTTCTACCTACGATGTGGCGTGGGGCG  
 AGAAACAGACGTCAATGTAACAGAGAGGGTGTGCGGTTCTACCTACGATGTGGC **T** GTCGTGGGGCG  
 G P G G A N S A Y M L R D S G L D I A V F E  
 GGGCCTGGGGAGCTAACTCCGCCTACATGCTGAGGGACTCCGGCTGGACATCGCTGTGTCGAG  
 GGGCCTGGGGAGCTAACTCCGCCTACATGCTGAGGGACTCCGGCTGGACATCGCTGTGTCGAG  
 GGGCCTGGGGAGCTAACTCCGCCTACATGCTGAGGGACTCCGGCTGGACATCGCTGTGTCGAG  
 Y S D **R** V G G R L F T Y Q I P N T P D V N L  
 TACTC **G** ACCGAGTGGCGGCCGGCTGTTCACCTACCACTGCCCCAACACACCCGACGTTAA **C** CTG  
 TACTCAGACCGAGTGGCGGCCGGCTGTTCACCTACCACTGCCCCAACACACCCGACGTTAACTC  
 TACTCAGACCGAGTGGCGGCCGGCTGTTCACCTACCACTGCCCCAACACACCCGACGTTAACTC  
 E I G G M R F I E G A M H R L W R V I S E L  
 GAGATTGGCGGCATGAGGTTCATCGA **A** GGCATGCACAGGCTCTGGAGGGTCATTCAGAACTC  
 GAGATTGGCGGCATGAGGTTCATCGAGGGCGCCATGCACAGGCTCTGGAGGGTCATTCAGAACTC  
 GAGATTGGCGGCATGAGGTTCATCGAGGGCGCCATGCACAGGCTCTGGAGGGTCATTCAGAACTC  
 G L T P K V F K E G F G K E G R Q R F Y L R  
 GGCCTAACCCCCAACGGTGTCAAGGAAGGTTGGC **A** AGGAGGGCAGACA **A** AGATTTCACCTGCGG  
 GGCCTAACCCCCAACGGTGTCAAGGAAGGTTGGC **A** AGGAGGGCAGACA **A** GAGATTTCACCTGCGG  
 GGCCTAACCCCCAACGGTGTCAAGGAAGGTTGGC **A** AGGAGGGCAGACA **A** GAGATTTCACCTGCGG  
 G Q S L T K K Q V K S G D V P Y D I S P E E  
 GGACAGAGCCTGACCAAGAACAGGTCAAGAGTGGGACGTACCCATGACCTCAGCCGGAGGAG  
 GGACAGAGCCTGACCAAGAACAGGTCAAGAGTGGGACGTACCCATGACCTCAGCCGGAGGAG  
 GGACAGAGCCTGACCAAGAACAGGTCAAGAGTGGGACGTACCCATGACCTCAGCCGGAGGAG  
 K E N Q G N L V E Y Y L E K L T G L **Q** L N G  
 AAAGAAAACCAGGGAAATCTGGTCGAATACTACCTGGAGAAACTGACAGGTCTACA **A** CTCAACGGC  
 AAAGAAAACCAGGGAAATCTGGTCGAATACTACCTGGAGAAACTGACAGGTCTACA **A** CTCAACGGC  
 AAAGAAAACCAGGGAAATCTGGTCGAATACTACCTGGAGAAACTGACAGGTCTA **A** ACTCAACGGC  
 E G P L K R E V A L K L T V P D G R F L Y D L  
 GAGCCGCTAACGTGAGGTTGCGCTTAAACTAACCGTGCCGGACGGCAGATTCTCTATGACCTC  
 GAACCGCTAACGTGAGGTTGCGCTTAAACTAACCGTGCCGGACGGCAGATTCTCTATGACCTC  
 G **G** ACCGCTAACGTGAGGTTGCGCTTAAACTAACCGTGCCGGACGGCAGATTCTCTATGACCTC  
 S F D E A M D L V A S P E G K E F T R D T H  
 TCGTTTGACGAAGCCATGGATCTGGTTGCCTCCCTGAGGGCAAAGAGTTACCCGAGACACGCAC  
 TCGTTTGACGAAGCCATGGATCTGGTTGCCTCCCTGAGGGCAAAGAGTTACCCGAGACACGCAC  
 TCGTTTGACGAAGCCATGG **A** CTTGGTTGCCTCCCTGAGGGCAAAGAGTTACCCGAGACACGCAC

Fig.

4C (continued)

V F T G E V T L **D** A S A V S L F D D H L G E  
 GTCTTCAC~~A~~GGAGAGGTACCCCTGGACGCGTCGGCTGTCTCCCTCTCGACGACCACCTGGGAGAG  
 GTCTTCACCGGAGAGGTACCCCTGG~~G~~CGCGTCGGCTGTCTCCCTCTCGACGACCACCTGGGAGAG  
 GTTTCACCGGAGA~~A~~GTACCCCTGGACGCGTCGGCTGTCTCCCTCTCGACGACCACCTGGGAGAG  
  
 D Y Y G S E I Y T L K E G L S S V P Q G L L  
 GACTACTATGGCAGTGAGATCTACACCCTAAAGGAAGGACTGTCTCCGTCCCACAAGGGCTCCTA  
 GACTACTA~~G~~GGCAGTGAGATCTACACCCTCAAGGAAGGACTGTCTCCGTCCC~~T~~CAAGGGCTCCTA  
 GACTACTATGGCAGTGAGATCTACACCCTAAAGGAAGGACTGTCTCCGTCCCACAAGGGCTCCTA  
  
 Q **A**T F L D A A D S N E F Y P N S H L K A L R  
 CAGGCTTTCTGGACGCCGAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA  
 CAGGCTTTCTGGACGCCGAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA  
 CAG~~A~~CTTTCTGGACGCCGAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA  
  
 R K T N G Q Y V L Y F E P T T S K D G Q T T  
 CGTAAGACCAACGGTCAGTATGTTCTTACTTTGAGCCCACCTCCAAGGATGGACAAACCACA  
 CGTAAGACCAACGGTCAGTATGTTCTTACTTTGAGCCCACCTCCAAGGATGGACAAACCACA  
 CGTAAGACCAACGGTCAGTATGTTCTTACTTTGAGCCCACCTCCAAGGATGGACAAACCACA  
  
 I N Y L E P L Q V V C A Q R V I L A M P V Y  
 ATCAACTATCTGGAACCCCTGCAGGTTGTGTGCACA~~A~~AGAGTCATCCTGGCCATGCCGGT~~A~~TAC  
 ATCAACTATCTGGAACCCCTGCAGGTTGTGTGCACAGAGAGTCAT~~T~~CTGGCCATGCCGGTCTAC  
 ATCAACTATCTGGAACCCCTGCAGGTTGTGTGCACAGAGAGTCATCCTGG~~C~~ATGCCGGTCTAC  
  
A L N Q L D W N Q L R N D R A T O A Y A A V  
 GCTCTGAACCAACT~~A~~GACTGGAATCAGCTCAGAAATGACCGAGCCACCCAGCGTACGCTGCCGT~~T~~  
 GCTCTCAACCAG~~T~~GGAT~~T~~GGAAATCAGCTCAGAAATGACCGAGCCACCCAGCGTACGCTGCCGTG  
 GCTCTCAACCAACTGGACTGGAATCAGCTCAGAAATGACCGAGCCACCCAGCGTACGCTGCCGTG  
  
R P I P A S K V F M T S F D O P W W L E N E R  
 CGCCCGATTCTGCAAGTAAGGTGTTCATG~~T~~CTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG  
 CGCCCGATTCTGCAAGTAAGGTGTTCATGACCTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG  
 CGCCCGATTCTGCAAGTAA~~A~~GTGTTCATGACCTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG  
  
K S W V T K S D A L F S O M Y D W Q K S E A  
 AAATCCTGGGTACCAAGTCGGACGCGCTTTCAGCCAAATGTACGACTGGCAGAAGTCTGAGGCG  
 AAATCCTGGGTACCAAGTCGGACGCGCTTTCAG~~T~~CAAATGTACGACTGGCAGAAGTCTGAGGCG  
 AAATCCTGGGTACCAAGTCGGACGCGCTTTCAGCCAAATGTACGACTGGCAGAAGTCTGAGGCG  
  
S G D Y I L I A S Y A D G I K A Q Y L R E L  
 TCCGGAGACTACATCCTGATGCCAGCTACGCCAGGGCTCAAAGCCAGTACCTGCAGGGAGCTG  
 TCCGGAGACTACATCCTGATGCCAGCTACGCCAGGGCTCAAAGCCAGTACCTGCAGGGAGCTG  
 TCCGGAGACTACATCCTGATGCCAGCTACGCCAGGGCTCAAAGCCAGTACCTGCAGGGAGCTG  
  
K N Q G E D I P G S D P G Y N Q V T E P L K  
 AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGT~~T~~ACCGAACCCCTCAAG  
 AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTACCGAACCCCTCAAG  
 AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTACCGAACCCCTCAAG

Fig.

## 4C (continued)

D T I L D H L T E A Y G V E R D S I **PR** E P V  
 GACACCATTCTGACCACCTCACTGAGGCTTATGGCGTGGAGCGAGACTCGAT**CCC**GGAAACCCGTG  
 GACACCATTCTGACCACCTCACTGAGGCTTATGGCGTGGAGCGAGACTCGAT**CC**GGAAACCCGTG  
 GACACCATTCTGACCACCTCACTGAGGCTTATGGCGTGG**A**CGAGACTCGAT**CCC**GGAAACCCGTG

T A A S Q F W T D Y P F G C G W I T W R A G  
 ACCGCCGCTTCCCAGTTCTGGACAGACTACCCGTTGGCTGTGGATGGATCACCTGGAGGGCCGGC  
 ACCGCCGCTTCCCAGTTCTGGACAGACTACCCGTTGGCTGTGGATGGATCACCTGGAGGGCCGGC  
 ACCGCCGCTTCCCAGTTCTGGAC**C**GA**T**ACCCGTT**C**GGCTGTGGATGGATCACCTGGAGGG**C**GGC

F H F D D V I S T M R R P S L K D E V Y V V  
 TTCCATTCGATGACGT**C**ATCAGCACCATGCGTCGCCGTCACTGAAAGATGAGGT**A**TACGTGGTG  
 TTCCATTCGATGACGT**C**ATCAGCACCATGCGTCGCCGTCACTGAAAGATGAGGT**C**TACGTGGTG  
 TTCCATT**T**GATGACGT**C**ATCAGCACCATGCGTCGCCGTCACTGAAAGATGAGGT**C**TACGTGGTG

G A D Y S W G L I S S W I E G A L E T S E N  
 GGAGCCGA**C**TACTCCTGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCTCGGAAAAC  
 GGAGCCGATTACTCCTGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCT**C**AGAAAAC  
 GGAGCCGATTACTCCTGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCTCGGAAAAC

V I N D Y F L -  
 GTCATCAACGACTACTTCCTCTAA  
 GTCATCAACGACTACTTCCTCTAA  
 GTCATCAACGACTACTTCCTCTAA

## 4D

VS

MSSAVLLLACALVISVHADGICRNRRQCNREVCGSTYD**VAVVGA**

^

^

^

^

10

20

30

40

T

Q

H

S

**GPGGANSA**YMLRD**SGLDIAVFEYSD**RVGGRLFT**YQLPNTPDVN**L

50

60

70

80

Fig.

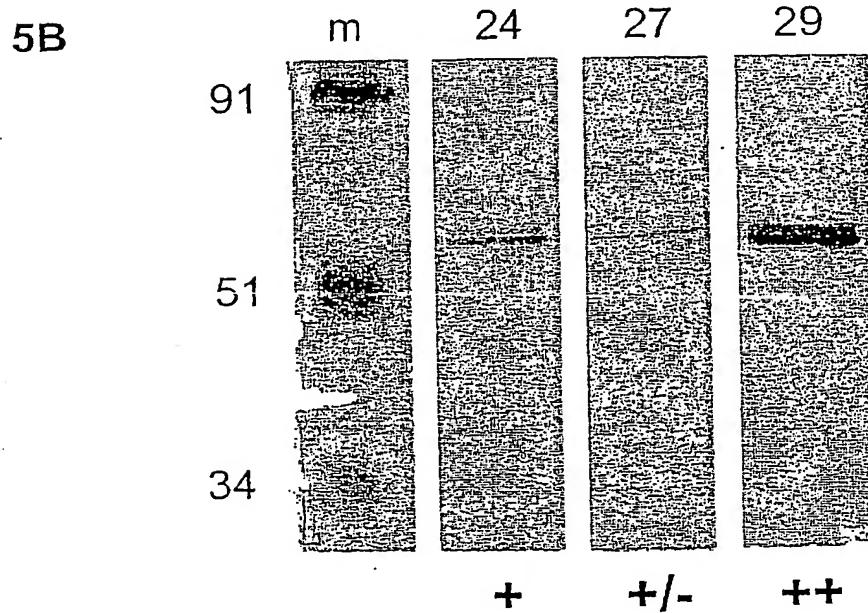
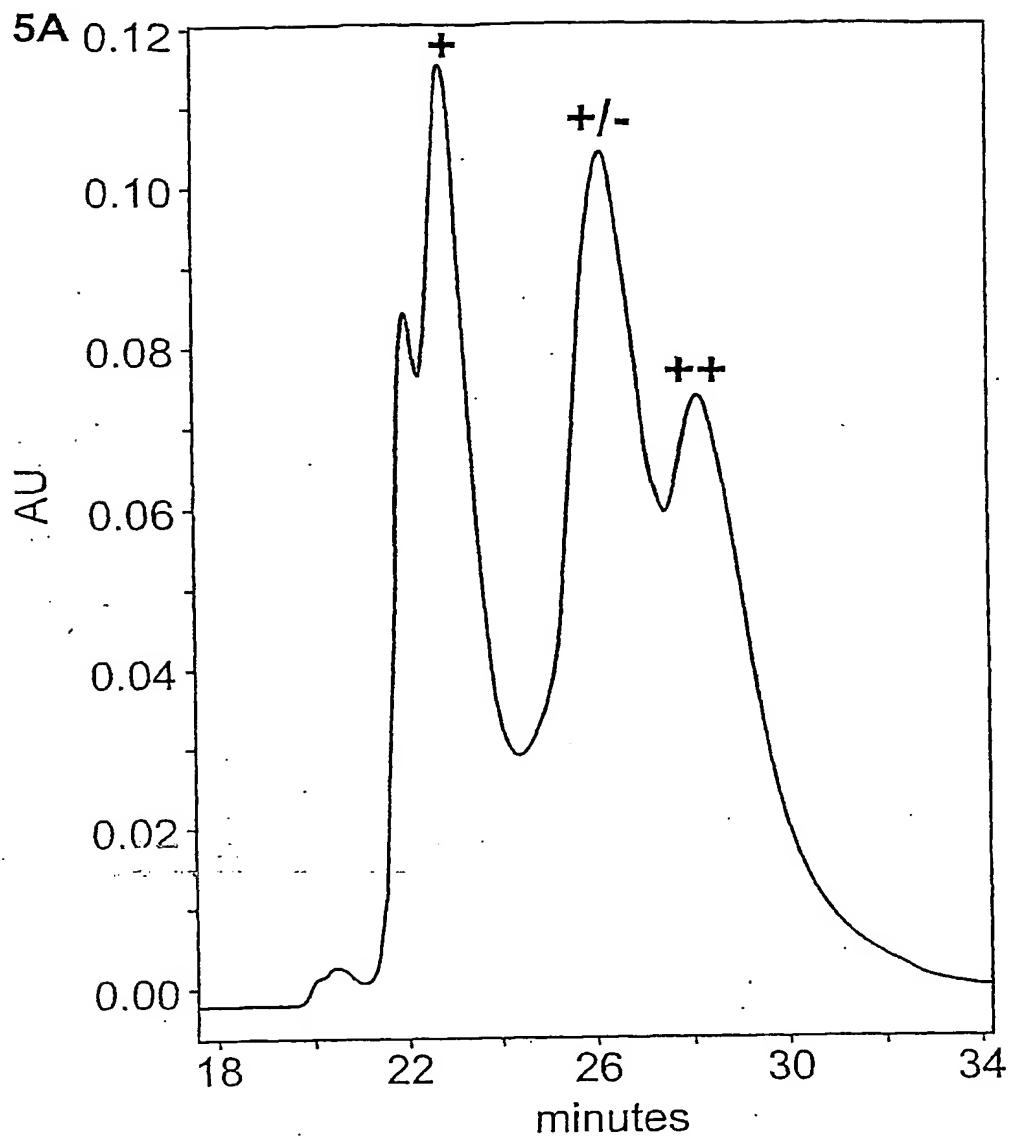


Fig.

5 C

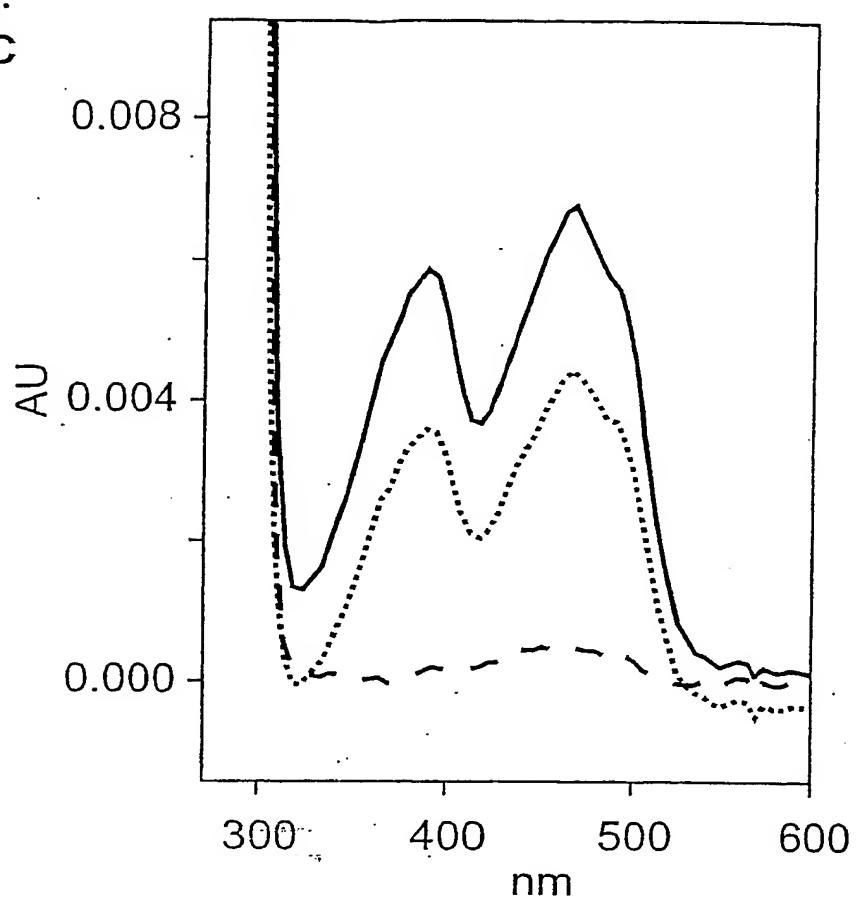
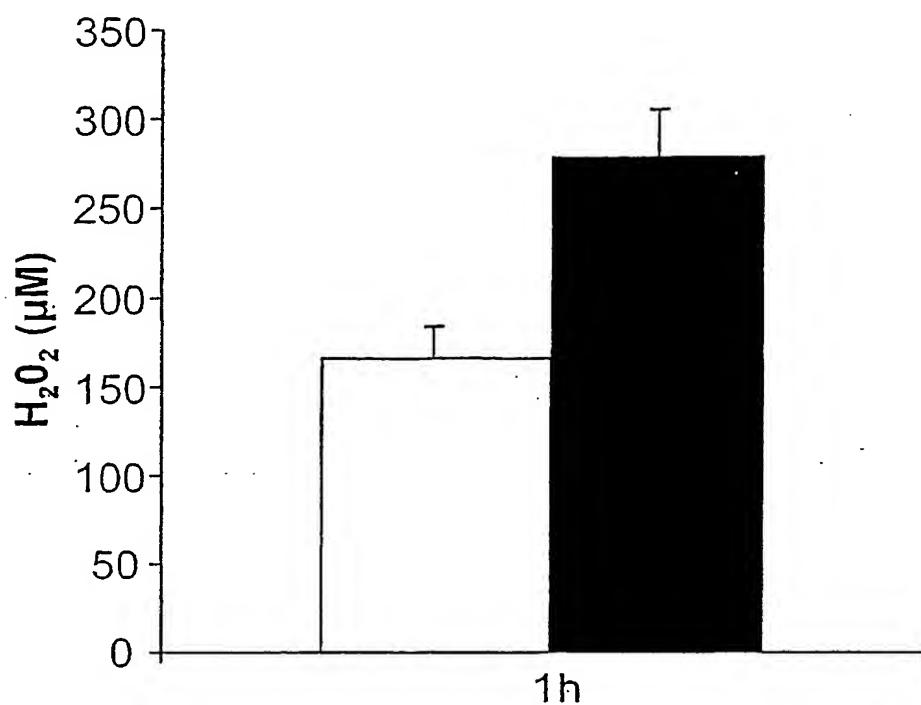
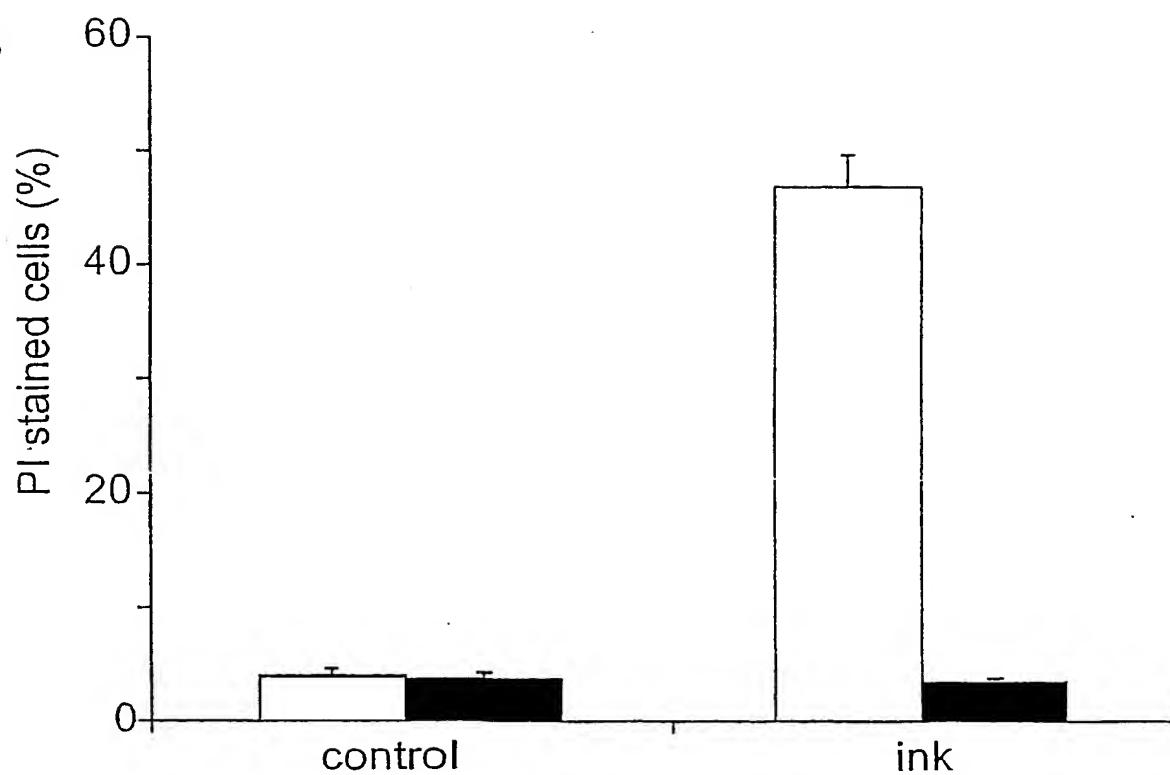


Fig.

6A



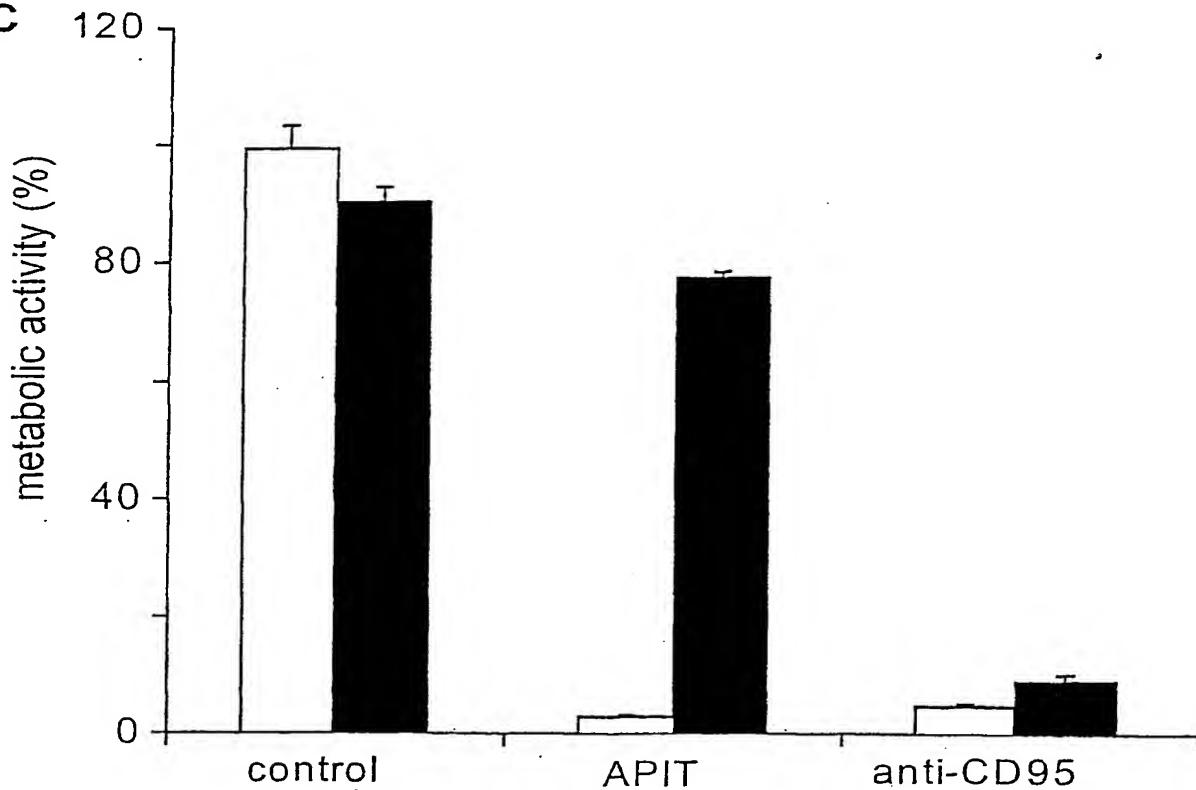
6B



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Fig.

6C



6D

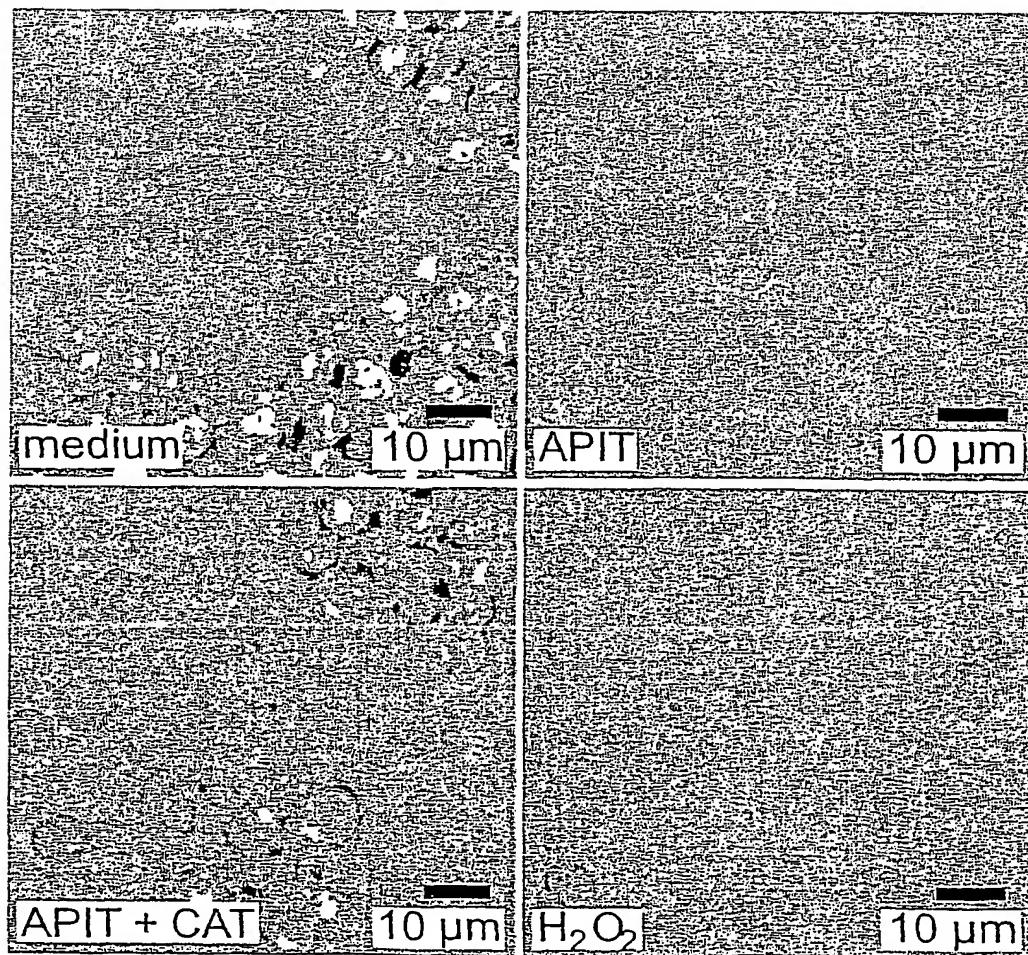


Fig. 6E

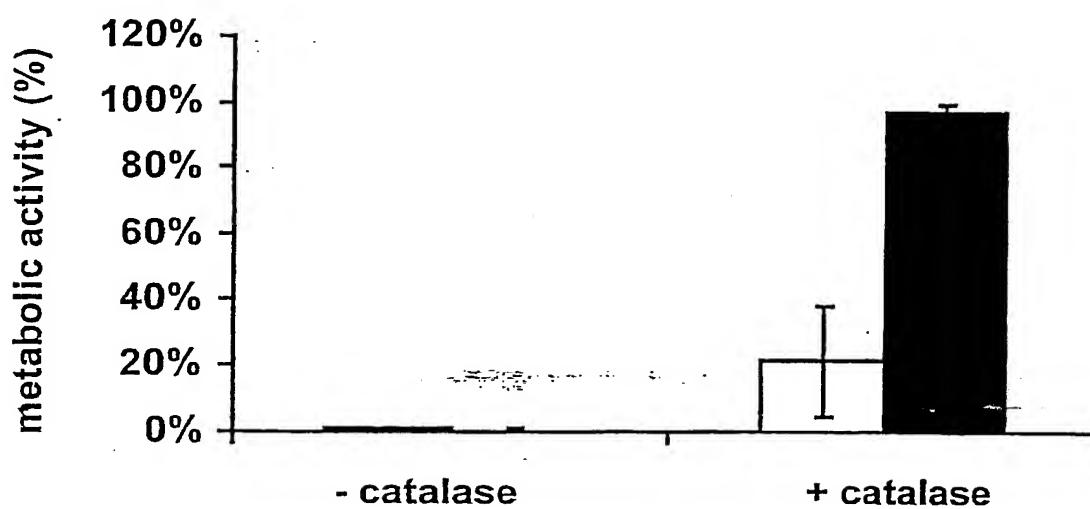
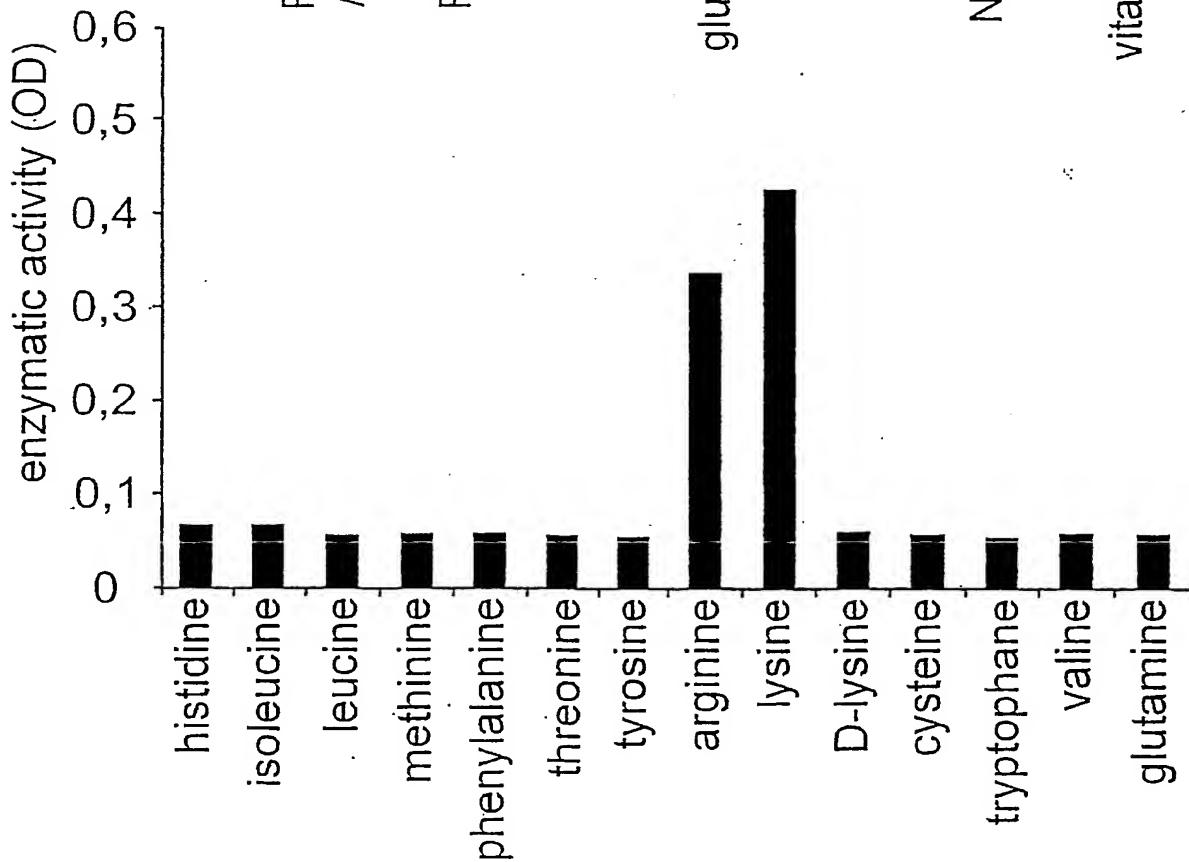
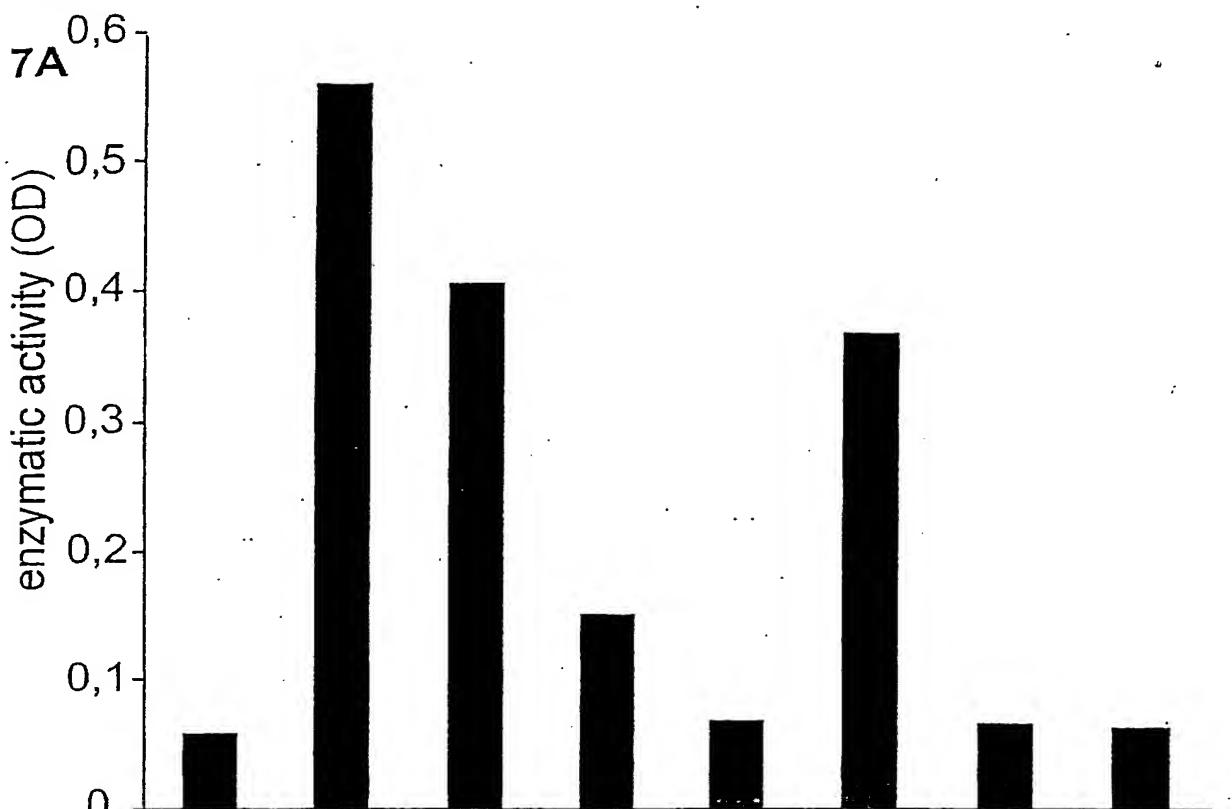
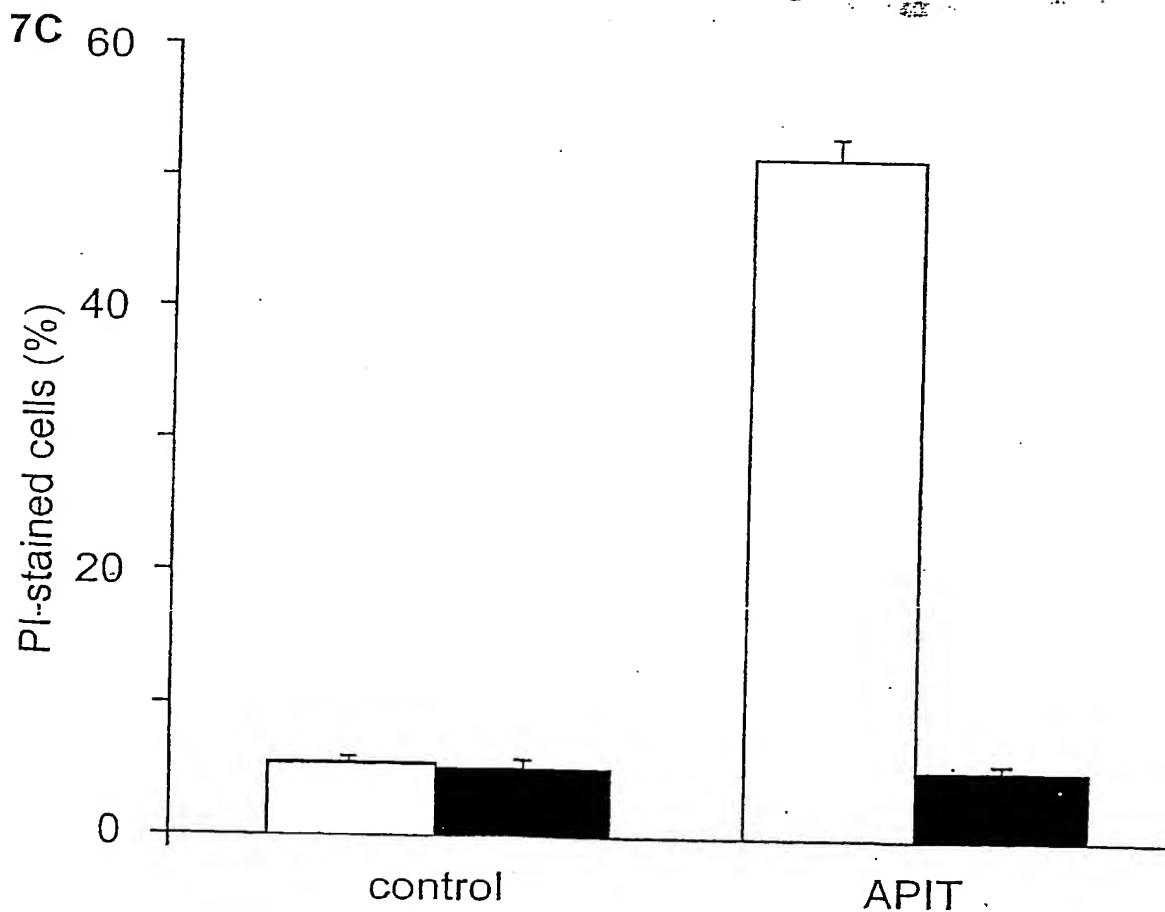
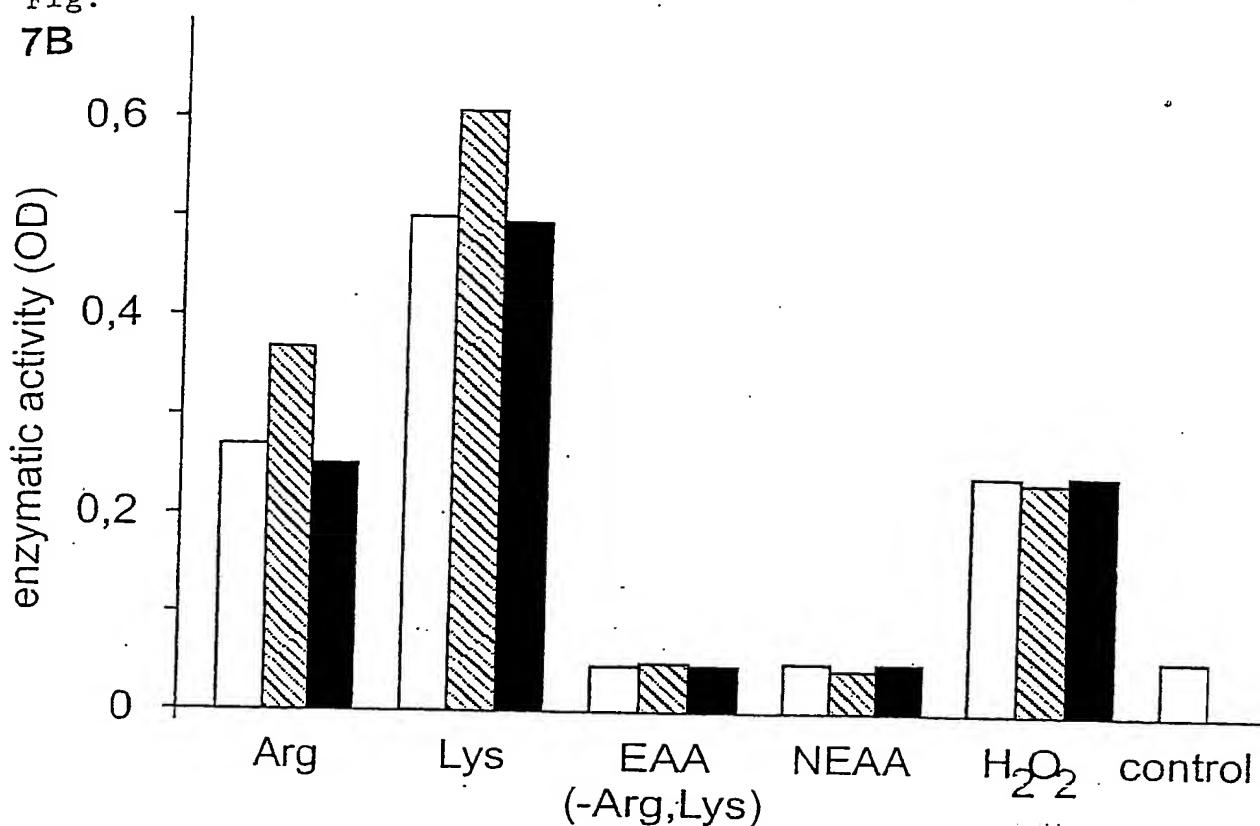
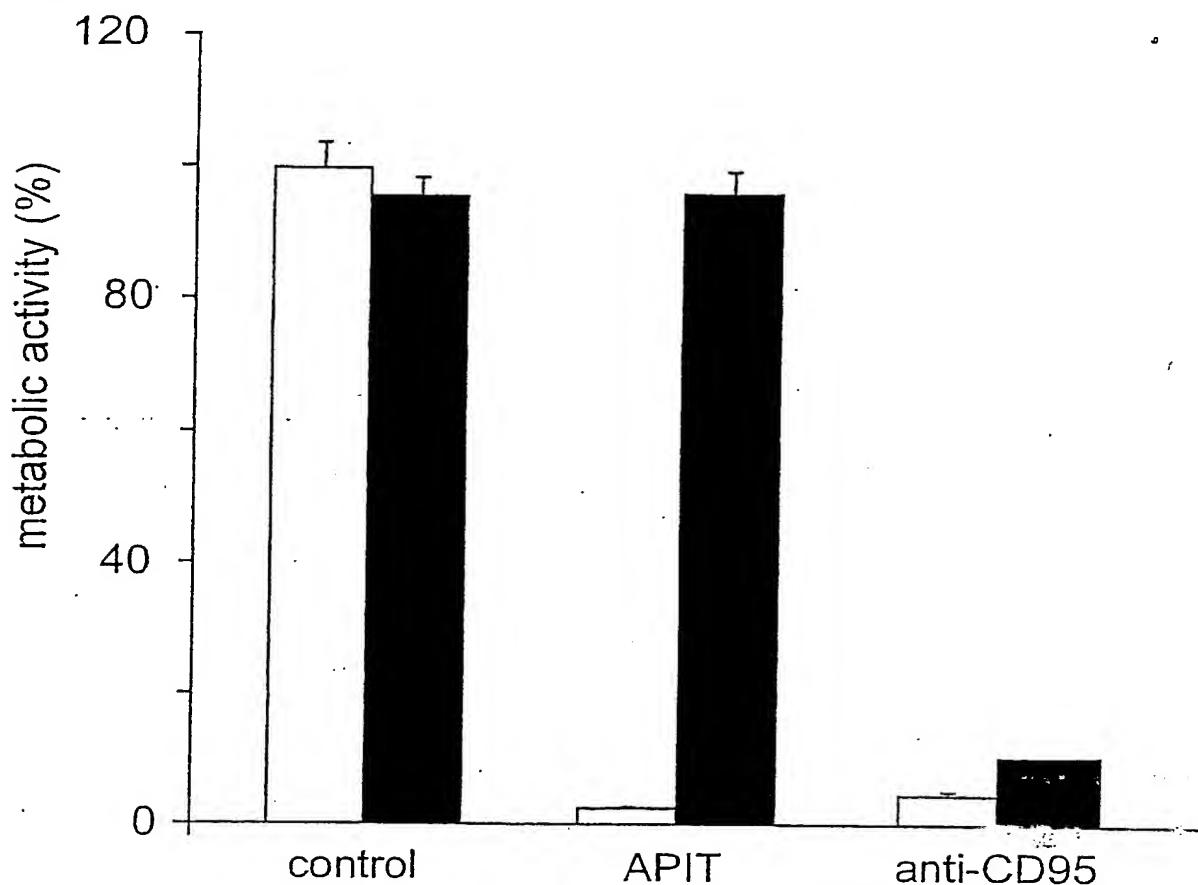


Fig.





7D



7E

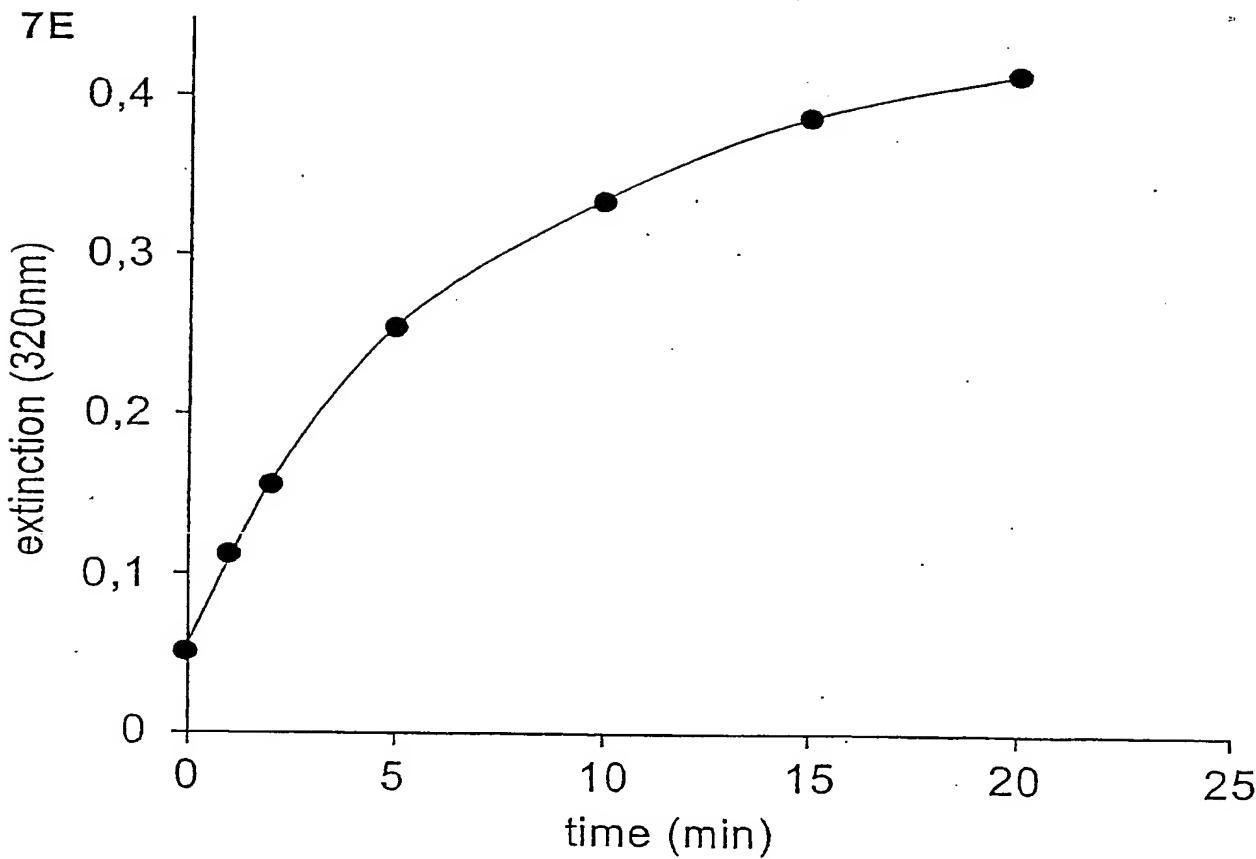
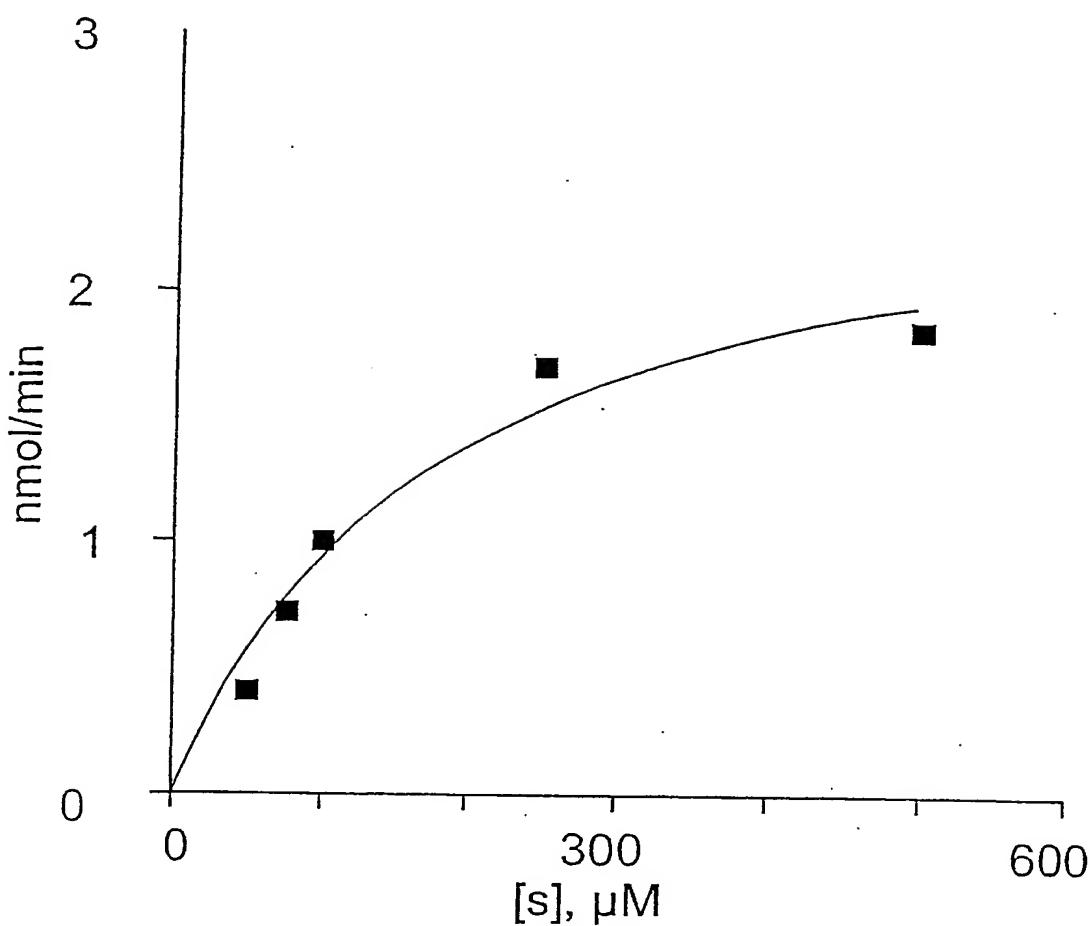
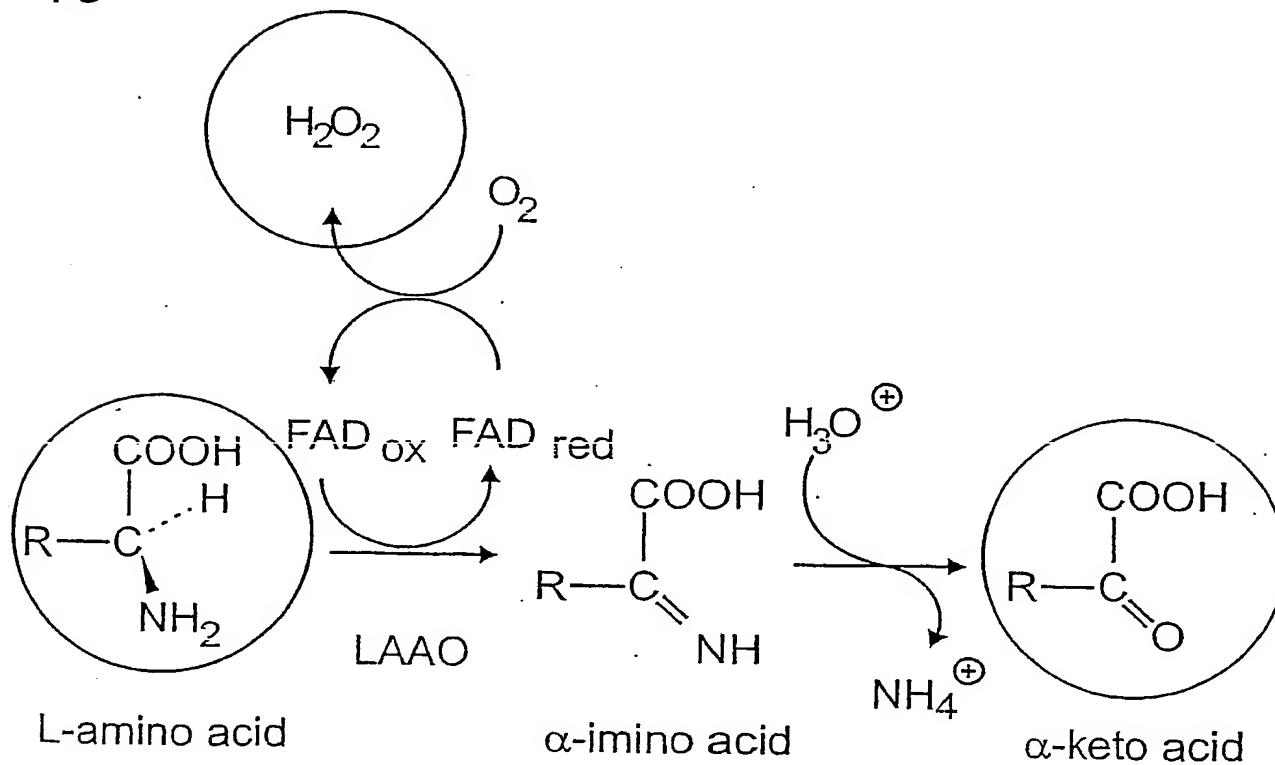


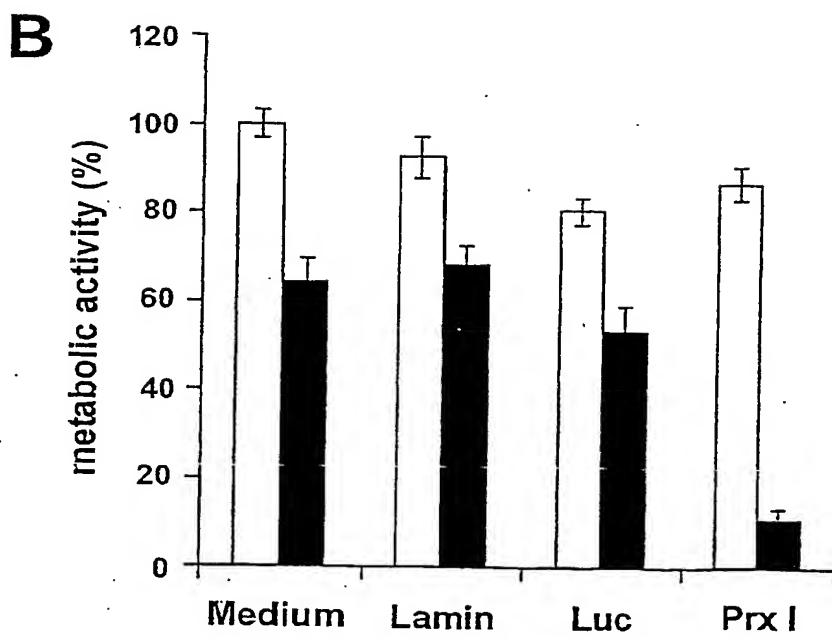
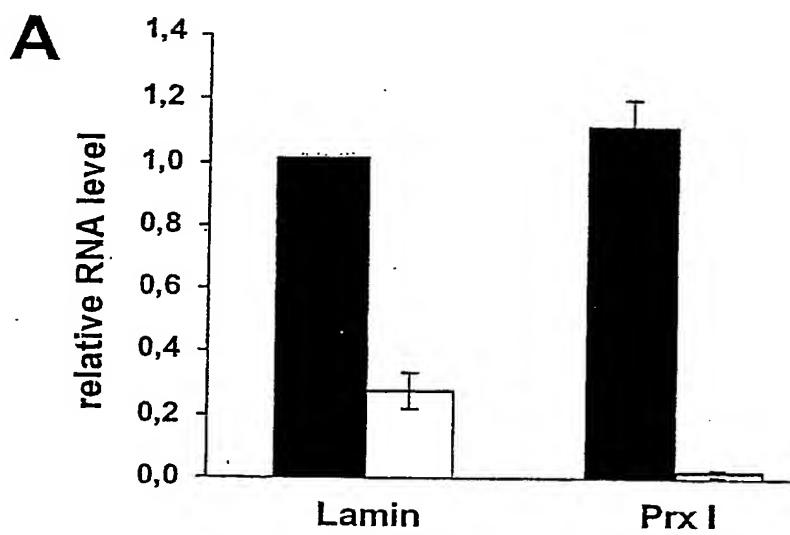
Fig.

7F

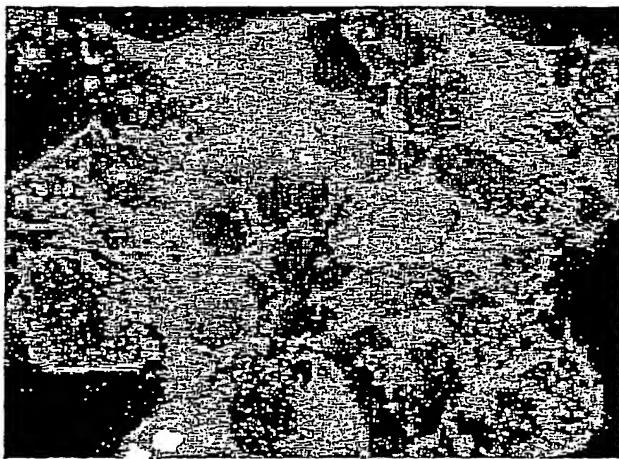
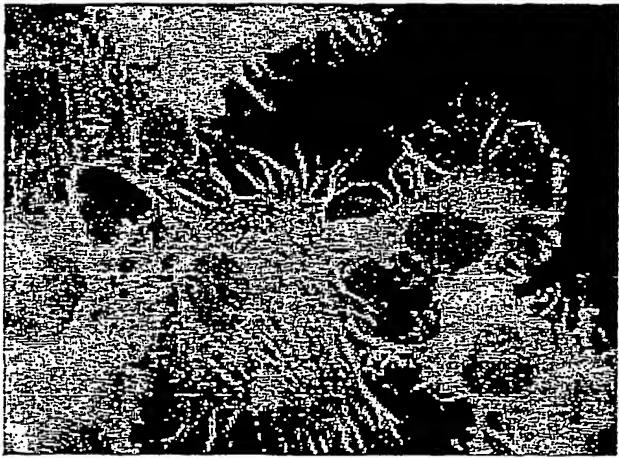


7G

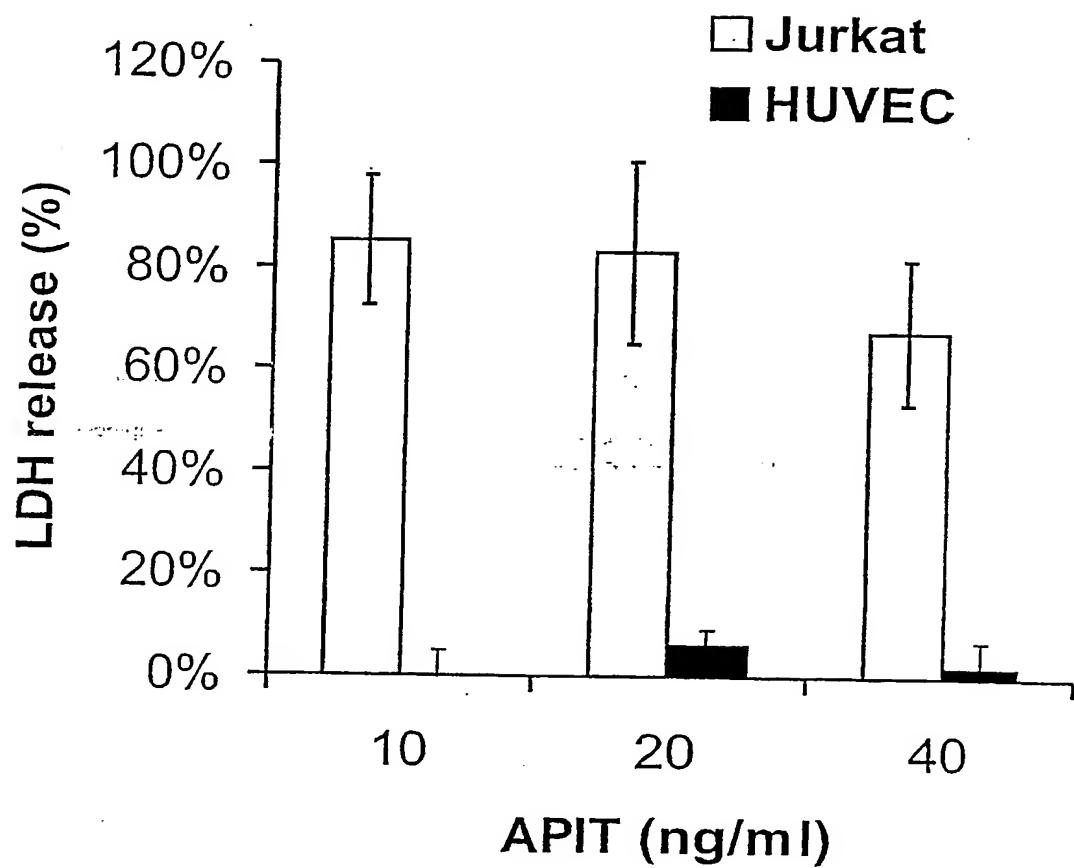


**Fig. 8**

# Fig. 9

**A****B****C**

# Fig. 10



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